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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C07K 14/00	A2	(11) International Publication Number: WO 98/54213 (43) International Publication Date: 3 December 1998 (03.12.98)
(21) International Application Number: PCT/US98/08486 (22) International Filing Date: 27 April 1998 (27.04.98) (30) Priority Data: 08/866,354 30 May 1997 (30.05.97) US (71) Applicant: AMGEN INC. [US/US]; Amgen Center, One Amgen Center Drive, Thousand Oaks, CA 91320-1789 (US). (72) Inventors: FOX, Gary, M.; 35 West Kelly Road, Newbury Park, CA 91320 (US). JING, Shuqian; 3254 Bordero Lane, Thousand Oaks, CA 91362 (US). WEN, Duanzhi; 517 Raindance Street, Thousand Oaks, CA 91360 (US). (74) Agents: ODRE, Steven, M. et al.; Amgen Inc., Amgen Center, One Amgen Center Drive, Thousand Oaks, CA 91320-1789 (US).		(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG). Published <i>Without international search report and to be republished upon receipt of that report.</i>
(54) Title: NEUROTROPHIC FACTOR RECEPTORS Human Glial Cell Line-Derived Neurotrophic Factor Receptor Protein 10 30 50 AATCTGGCCTCGGAACACGCCATTCTCCGCGCCGCTTCCAATAACCACTAACATCCCTA 70 90 110 ACGAGCATCCGAGCCGAGGGCTCTGCTCGGAAATCGTCCTGGCCCAACTCGGCCCTTCGA 130 150 170 GCTCTCGAAGATTACCGCATCTATTTTTTTTTTCTTTTTTTTCTTTTCCTAGCGCAGATA		
(57) Abstract The present invention relates to glial cell line-derived neurotrophic factor (GDNF), a potent neurotrophin that exhibits a broad spectrum of biological activities on a variety of cell types from both the central and peripheral nervous systems. The present invention involves the cloning and characterization of receptors for GDNF. Nucleic acid and amino acid sequences are described for GDNFR protein products. A hydrophobic domain with the features of a signal peptide is found at the amino terminus, while a second hydrophobic domain at the carboxy terminus is involved in the linkage of the receptor to the cell membrane. The lack of a transmembrane domain and cytoplasmic region indicates that GDNFR requires one or more accessory molecules in order to mediate transmembrane signaling. GDNFR mRNA is widely distributed in both nervous system and non-neural tissues, consistent with the similar distribution found for GDNF.		

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NEUROTROPHIC FACTOR RECEPTORS

1. Field of the Invention

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The present invention relates to receptors for neurotrophic factors. In particular, the invention relates to receptors for glial cell line-derived neurotrophic factor (GDNF) and neurturin and provides nucleic acid and amino acid sequences encoding the receptors. The present invention also relates to therapeutic techniques for the treatment of neurotrophic factors-responsive conditions.

2. Background of the Invention

Glial Cell line-Derived Neurotrophic Factor

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Glial cell line-derived neurotrophic factor (GDNF) was initially isolated and cloned from rat B49 cells as a potent neurotrophic factor that enhances survival of midbrain dopaminergic neurons (Lin et al., Science, 260, 1130-1132, 1993). Recent studies have indicated that this molecule exhibits a variety of other biological activities, having effects on several types of neurons from both the central and peripheral nervous systems. In the central nervous system (CNS), GDNF has been shown to prevent the axotomy-induced death of mammalian facial and spinal cord motor neurons (Li et al., Proceedings Of The National Academy Of Sciences, U.S.A., 92, 9771-9775, 1995; Oppenheim et al., Nature, 373, 344-346, 1995; Yan et al., Nature, 373, 341-344, 1995; Henderson et al., Science, 266, 1062-1064, 1994; Zurn et al., Neuroreport, 6, 113-118, 1994), and to rescue developing avian motor neurons from natural programmed cell death (Oppenheim et al., 1995 supra). Local administration of GDNF has been shown to protect nigral dopaminergic neurons from axotomy-induced (Kearns and Gash, Brain Research, 672, 104-111, 1995; Beck et al., Nature, 373, 339-341, 1995) or neurotoxin-induced degeneration (Sauer et al., Proceedings Of The National Academy Of Sciences U.S.A., 92, 8935-8939, 1995; Tomac et al., Nature, 373, 335-339, 1995). In addition, local administration of GDNF has been shown to induce sprouting from dopaminergic neurons, increase levels of dopamine, noradrenaline, and serotonin, and improve motor behavior (Tomac et al., 1995 supra).

35

More recently, GDNF has been reported to be a potential trophic factor for brain noradrenergic neurons and Purkinje cells. Grafting of fibroblasts ectopically expressing GDNF prevented 6-hydroxydopamine-induced degeneration and

promoted the phenotype of adult noradrenergic neurons in vivo (Arenas et al., Neuron, 15, 1465-1473, 1995), while exogenously applied GDNF effectively promoted survival and morphological differentiation of embryonic Purkinje cells in vitro (Mount et al., Proceedings Of The National Academy Of Sciences U.S.A., 92, 9092-9096, 1995). In the peripheral nervous system, GDNF has been shown to promote the survival of neurons in nodose, ciliary, and sympathetic ganglia, as well as small populations of embryonic sensory neurons in dorsal root ganglia (DRG) and trigeminal ganglia (Trupp et al., Journal Of Cell Biology, 130, 137-148, 1995; Ebendal et al., Journal Of Neuroscience Research, 40, 276-284, 1995; Oppenheim et al., 1995 supra; Yan et al., 1995 supra; Henderson et al., 1994 supra). GDNF has also been reported to enhance the expression of vasoactive intestinal peptide and preprotachykinin-A mRNA in cultured superior cervical ganglion (SCG) neurons, and thus effects the phenotype of SCG neurons and induces bundle-like sprouting (Trupp et al., 1995 supra).

Expression of GDNF has been observed in a number of different cell types and structures of the nervous system. In the CNS, GDNF mRNA expression has been observed by reverse transcriptase polymerase chain reaction (RT-PCR) in both developing and adult rat striatum, the major target of nigral dopaminergic innervation, and widely in other regions, including hippocampus, cortex, thalamus, septum, cerebellum, spinal cord, and medulla oblongata (Arenas et al., supra 1995; Poulsen et al., Neuron, 13, 1245-1252, 1994; Springer et al., Experimental Neurology, 127, 167-170, 1994; Stroemberg et al., Experimental Neurology, 124, 401-412, 1993; Schaar et al., Experimental Neurology, 124, 368-371, 1993). In human, GDNF transcripts have also been detected in striatum, with highest level in the caudate and lower levels in the putamen. Detectable levels are also found in hippocampus, cortex, and spinal cord, but not in cerebellum (Schaar et al., Experimental Neurology, 130, 387-393, 1994; Springer et al., 1994 supra). In the periphery, GDNF mRNA expression has been reported in DRG and SCG of postnatal day 1 rats, sciatic nerve, and primary cultures of neonatal Schwann cells (Trupp et al., 1995 supra; Hoffer et al., Neuroscience Letters, 182, 107-111, 1994; Henderson et al., 1994 supra; Springer et al., 1994 supra). In addition, recent studies have shown that GDNF transcripts are also widely expressed in peripheral non-neuronal organs, including postnatal testis and kidney, embryonic whisker pad, stomach, and skin. Expression can be detected at lower levels in embryonic muscle, adrenal gland and limb bud, and in postnatal lung, liver and ovary (Trupp et al., 1995 supra; Henderson et al., 1994 supra). So far, however, the biological significance of the non-neuronal expression of GDNF is not clear.

A neurotrophic factor referred to as "neurturin" is described in Nature 384(5):467-470, 1996. Detailed descriptions of the preparation and characterization of GDNF protein products may be found in U.S. Patent Application No. 08/182,183 filed May 23, 1994 and its parent applications (also see PCT/US92/07888, WO 93/06116 filed September 17, 1992 and European Patent Application No. 92921022.7, Publication No. EP 610 254) the disclosures of which are hereby incorporated by reference. Additional GDNF protein products are described in pending U.S. Patent Application No. 08/535,681 filed September 28, 1995, the disclosure of which is hereby incorporated by reference. As used herein, the term "GDNF protein product" includes biologically active synthetic or recombinant GDNF proteins and analogs, as well as chemically modified derivatives thereof. GDNF analogs include deletion variants such as truncated GDNF proteins, as well as insertion and substitution variants of GDNF. Also included are GDNF proteins that are substantially homologous to the human GDNF protein.

15

GDNF Therapy

GDNF therapy is helpful in the treatment of nerve damage caused by conditions that compromise the survival and/or proper function of one or more types of nerve cells. Such nerve damage may occur from a wide variety of different causes. Nerve damage may occur to one or more types of nerve cells by: (1) physical injury, which causes the degeneration of the axonal processes and/or nerve cell bodies near the site of injury; (2) temporary or permanent cessation of blood flow to parts of the nervous system, as in stroke; (3) intentional or accidental exposure to neurotoxins, such as chemotherapeutic agents (e.g., cisplatin) for the treatment of cancer or dideoxycytidine (ddC) for the treatment of AIDS; (4) chronic metabolic diseases, such as diabetes or renal dysfunction; or (5) neurodegenerative diseases such as Parkinson's disease, Alzheimer's disease, and amyotrophic lateral sclerosis (ALS), which result from the degeneration of specific neuronal populations.

Several studies indicate that GDNF therapy is particularly helpful in the treatment of neurodegenerative conditions such as the degeneration of the dopaminergic neurons of the substantia nigra in Parkinson's disease. The only current treatments for Parkinson's disease are palliative, aiming at increasing dopamine levels in the striatum. The expected impact of GDNF therapy is not simply to produce an increase in the dopaminergic neurotransmission at the dopaminergic nerve terminals in the striatum (which will result in a relief of the symptoms), but also to slow down, or even stop, the progression of the degenerative processes and to repair the damaged nigrostriatal pathway and restore its function.

GDNF may also be used in treating other forms of damage to or improper function of dopaminergic nerve cells in human patients. Such damage or malfunction may occur in schizophrenia and other forms of psychosis. The only current treatments for such conditions are symptomatic and require drugs which act upon dopamine
5 receptors or dopamine uptake sites, consistent with the view that the improper functioning of the dopaminergic neurons which innervate these receptor-bearing neuronal populations may be involved in the disease process.

Receptors

10 A number of receptors which mediate binding and response to protein factors have been characterized and molecularly cloned, including receptors for insulin, platelet derived growth factor, epidermal growth factor and its relatives, the fibroblast growth factors, various interleukins, hematopoietic growth factors and ciliary neurotrophic factor (U.S. 5,426,177). Study results indicate that some
15 receptors can bind to multiple (related) growth factors, while in other cases the same factor can bind and activate multiple (related) receptors (e.g., Lupu et al., Science, 249:1552-1555, 1990; Dionne et al., EMBO J., 9:2685-2692, 1990; Miki et al., Science, 251:72-75, 1991). Most receptors can broadly be characterized as having an extracellular portion or domain responsible for specifically binding a protein
20 factor, a transmembrane domain which spans the cell membrane, and an intracellular domain that is often involved in initiating signal transduction upon binding of the protein factor to the receptor's extracellular portion. Although many receptors are comprised of a single polypeptide chain, other receptors apparently require two or more separate subunits in order to bind to their protein factor with high-affinity and
25 to allow functional response following binding (e.g., Hempstead et al., Science, 243:373-375, 1989; Hibi et al., Cell, 63:1149-1157, 1990).

The extracellular and intracellular portions of a given receptor may share common structural motifs with the corresponding regions of other receptors, suggesting evolutionary and functional relationships between different receptors.
30 These relationships can often be quite distant and may simply reflect the repeated use of certain general domain structures. For example, a variety of different receptors that bind unrelated factors make use of "immunoglobulin" domains in their extracellular portions, while other receptors utilize "cytokine receptor" domains in their factor-binding regions (e.g., Akira et al., The FASEB J., 4:2860-2867, 1990).
35 A large number of receptors with distinct extracellular binding domains (which thus bind different factors) contain related intracytoplasmic domains encoding tyrosine-specific protein kinases that are activated in response to factor binding (e.g., Ullrich

and Schlessinger, Cell, 61:203-212, 1990). The mechanisms by which factor-binding "activates" the signal transduction process is poorly understood, even in the case of receptor tyrosine kinases. For other receptors, in which the intracellular domain encodes a domain of unknown function or in which the binding component associates with a second protein of unknown function (e.g., Hibi et al., Cell, 63:1149-1157, 1990), activation of signal transduction is not well characterized.

The mode of action of GDNF *in vivo* is not clearly elucidated in the art, in part due to the absence of information on a receptor for GDNF. Two groups have independently found that striatum injected [125 I]-labeled GDNF can be retrogradely transported by dopaminergic neurons in the substantia nigra (Tomic et al., Proceedings Of The National Academy Of Sciences Of The United States Of America. 92, 8274-8278, 1995; Yan et al., 1995 *supra*). Retrograde transport of [125 I]-GDNF by spinal cord motor neurons, DRG sensory neurons and neurons in the B layer of retina ganglia was also been observed. These retrograde transport phenomena can all be specifically inhibited by 100-fold or higher concentrations of unlabeled GDNF, suggesting a saturable, receptor-mediated transport process. *In vitro*, recombinant GDNF has been shown to enhance the survival and promote dopamine uptake of cultured dopaminergic neurons at very low concentrations. The observed half-maximal effective concentration (EC_{50}) of GDNF on these neurons is 0.2 to 1.6 pM (Lin et al., 1993 *supra*). GDNF has also been shown to support the survival of dissociated motor neurons at low concentrations. The reported EC_{50} of GDNF on motor neurons, in a 5 to 10 fM range, is even lower than that on dopaminergic neurons (Henderson et al., 1994 *supra*).

Taken together, these observations indicate that receptor(s) for GDNF expressed in these cells have very high ligand binding affinities. Similar to members of the TGF- β family, the widely diversified tissue distribution and varied biological function of GDNF on different populations of cells suggest that different types of receptor(s) for GDNF or receptor complexes may exist. Saturation steady-state and competitive binding of [125 I]-GDNF to E10 chick sympathetic neurons has shown that these neurons express GDNF binding sites differing from those observed in dopaminergic and motor neurons. The half maximal saturation concentration and the half-maximal inhibition concentration of GDNF on these binding sites is in the range of 1 to 5 nM (Trupp et al., 1995 *supra*). Similarly, the EC_{50} of GDNF in supporting the survival of sympathetic neurons from P1 rat SCG has also been reported to be in the nanomolar range (Trupp et al., 1995 *supra*).

To better understand the mechanism by which GDNF activates signal transduction to exert its effects on cells, it would be beneficial to identify the

receptor(s) which mediate binding and response to this protein factor. It would also be beneficial for GDNF therapy to identify and make possible the production of accessory molecules which provide for or enhance GDNF signal transduction. Moreover, the identification of a protein receptor for GDNF would provide powerful applications in diagnostic uses, for example, as an aid in determining if individuals would benefit from GDNF protein therapy. Furthermore, the protein receptor for GDNF could be a key component in an assay for identifying additional molecules which bind to the receptor and result in desired biological activity.

10

SUMMARY OF THE INVENTION

The present invention provides nucleic acid sequences which encode neurotrophic factor receptor proteins having amino acid sequences as depicted in the Figures as well as biologically equivalent analogs. The neurotrophic factor receptor protein and protein products of the present invention are designated herein as glial cell line-derived neurotrophic factor receptor (GDNFR) protein and protein products. Particular receptor proteins referred to herein include GDNFR- α , and glial cell line-derived neurotrophic factor receptor- α -related receptor proteins 2 and 3 (GRR2 and GRR3). The novel proteins are functionally characterized by the ability to bind GDNF and/or neurturin specifically, and to act as part of a molecular complex which mediates or enhances the signal transduction effects of GDNF and/or neurturin. GDNFR protein products are typically provided as a soluble receptor protein and in a substantially purified form.

25 In one aspect, the present invention provides for the production of GDNFR protein products by recombinant genetic engineering techniques. In an alternative embodiment, the GDNFR proteins are synthesized by chemical techniques, or a combination of the recombinant and chemical techniques.

30 In another aspect of the present invention, the GDNFR proteins may be made in glycosylated or non-glycosylated forms. Derivatives of GDNFR protein typically involve attaching the GDNFR protein to a water soluble polymer. For example, the GDNFR protein may be conjugated to one or more polyethylene glycol molecules to decrease the precipitation of the GDNFR protein product in an aqueous environment.

35 Yet another aspect of the present invention includes the various polynucleotides encoding GDNFR proteins. These nucleic acid sequences are used in the expression of GDNFR in a eukaryotic or prokaryotic host cell, wherein the expression product or a derivative thereof is characterized by the ability to bind to

GDNF and thereby form a complex capable of mediating GDNF activity, such as increasing dopamine uptake by dopaminergic cells. The polynucleotides may also be used in cell therapy or gene therapy applications. Suitable nucleic acid sequences include those specifically depicted in the Figures as well as degenerate sequences, naturally occurring allelic variations and modified sequences based on the present invention.

Exemplary nucleic acid sequences include sequences encoding a neurotrophic factor receptor protein comprising an amino acid sequence as depicted in the Figures capable of complexing with glial cell line-derived neurotrophic factor (GDNF) and/or neurturin and mediating cell response to GDNF and/or neurturin, and biologically equivalent analogs thereof. Such sequences include: (a) a sequence set forth in Figure 1 (SEQ ID NO. 1) comprising nucleotides encoding Met¹ through Ser⁴⁶⁵ or Figure 3 (SEQ ID NO. 3) comprising nucleotides encoding Met¹ through Ser⁴⁶⁸ encoding a neurotrophic factor receptor (GDNFR- α) capable of complexing with glial cell line-derived neurotrophic factor (GDNF) and mediating cell response to GDNF, as well as GRR2 and GRR3; (b) a nucleic acid sequence which (1) hybridizes to a complementary sequence of (a) and (2) encodes an amino acid sequence with GDNFR activity; and (c) a nucleic acid sequence which but for the degeneracy of the genetic code would hybridize to a complementary sequence of (a) and (2) encodes an amino acid sequence with GDNFR activity. Also disclosed herein are vectors such nucleic acid sequences wherein the sequences typically are operatively linked to one or more operational elements capable of effecting the amplification or expression of the nucleic acid sequence. Host cells containing such vectors are also contemplated. Typically, the host cell is selected from mammalian cells and bacterial cells, such as a COS-7 cell or E. coli, respectively.

A further aspect of the present invention involves vectors containing the polynucleotides encoding GDNFR proteins operatively linked to amplification and/or expression control sequences. Both prokaryotic and eukaryotic host cells may be stably transformed or transfected with such vectors to express GDNFR proteins. The present invention further includes the recombinant production of a GDNFR protein wherein such transformed or transfected host cells are grown in a suitable nutrient medium, and the GDNFR protein expressed by the cells is, optionally, isolated from the host cells and/or the nutrient medium. The present invention further includes the use of polynucleotides encoding GDNFR protein and vectors containing such polynucleotides in gene therapy or cell therapy.

The host cell may also be selected for its suitability to human implantation, wherein the implanted cell expresses and secretes a neurotrophic factor receptor of

the present invention. The host cell also may be enclosed in a semipermeable membrane suitable for human implantation. The host cell may be transformed or transfected ex vivo. An exemplary device for treating nerve damage involves: (a) a semipermeable membrane suitable for implantation; and (b) cells encapsulated
5 within the membrane, wherein the cells express and secrete a neurotrophic factor receptor as disclosed herein. The membrane is selected from a material that is permeable to the neurotrophic factor receptor protein but impermeable to materials detrimental to the encapsulated cells.

Methods for the recombinant production of a neurotrophic factor receptor of
10 the present invention are also disclosed. An exemplary method involves: (a) culturing a host cell containing a nucleic acid sequence encoding a GDNFR protein of the present invention, such as an amino acid sequence depicted in the Figures capable of complexing with glial cell line-derived neurotrophic factor and/or neurturin and mediating cell response to GDNF and/or neurturin, or biologically
15 equivalent analogs thereof; (b) maintaining said host cell under conditions suitable for the expression of said neurotrophic factor receptor by said host cell; and (c) optionally, isolating said neurotrophic factor receptor expressed by said host cell. The host cell may be a prokaryotic cell or a eukaryotic cell. If bacterial expression is involved, the method may further include the step of refolding the neurotrophic
20 factor receptor.

The present invention includes an isolated and purified protein comprising an amino acid sequence as depicted in the Figures capable of complexing with glial cell line-derived neurotrophic factor and/or neurturin and mediating cell response to GDNF and/or neurturin, and biologically equivalent analogs thereof. Exemplary
25 analogs include, but are not limited to, proteins comprising the amino acid sequence Ser¹⁸ through Pro⁴⁴⁶, Asp²⁵ through Leu⁴⁴⁷ and Cys²⁹ through Cys⁴⁴² as depicted in Figure 2 (SEQ ID NO:2) as well as proteins comprising the amino acid sequence Met¹⁷ through Pro⁴⁴⁹ and Cys²⁹ through Cys⁴⁴³ as depicted in Figure 4 (SEQ ID NO:4). The proteins of the present invention may be glycosylated or non-
30 glycosylated and may be produced by recombinant technology or chemical synthesis. The present invention further includes nucleic acid sequences encoding a receptor protein comprising such amino acid sequences.

Also disclosed herein are pharmaceutical compositions comprising a GDNFR protein of the present invention in combination with a pharmaceutically acceptable
35 carrier. A variety of other formulation materials may be used to facilitate manufacture, storage, handling, delivery and/or efficacy.

Another aspect of the present invention includes the therapeutic use of

5 GDNFR genes and proteins. For example, a circulating or soluble GDNFR protein product may be used alone or in conjunction with GDNF and/or neurturin in treating disease of or injury to the nervous system by enhancing the activity of transmembrane signaling of GDNF and/or neurturin. Thus, the proteins and pharmaceutical compositions of the present invention may be used in treating improperly functioning dopaminergic nerve cells, Parkinson's disease, Alzheimer's disease and amyotrophic lateral sclerosis. Alternatively, a recombinant GDNFR gene may be inserted in the cells of tissues which would benefit from increased sensitivity to GDNF or neurturin, such as motor neurons in patients suffering from amyotrophic lateral sclerosis. In yet another embodiment, GDNFR may be used to block GDNF or neurturin activity in cases where the GDNF or neurturin activity is thought to be detrimental. The GDNFR protein may be used to verify that observed effects of GDNF or neurturin are due to the GDNFR protein.

15 In another aspect of the invention, GDNFR probes may be used to identify cells and tissues which are responsive to GDNF or neurturin in normal or diseased states. Alternatively, the probes may be used to detect an aberrancy of GDNFR protein expression in a patient suffering from a GDNF- or neurturin-related disorder.

20 In a further aspect of the invention, GDNFR probes, including nucleic acid as well as antibody probes, may be used to identify GDNFR-related molecules. For example, the present invention provides for such molecules which form a complex with GDNFR protein and thereby participate in GDNFR protein function. As another example, the present invention provides for receptor molecules which are homologous or cross-reactive antigenically, but not identical to GDNFR- α , GRR2 or GRR3, including consensus sequence molecules as depicted in the Figures.

25 The present invention also provides for the development of both binding and functional assays for GDNF or neurturin based on the receptor. For example, assay systems for detecting GDNF activity may involve cells which express high levels of GDNFR- α , and which are therefore extremely sensitive to even very low concentrations of GDNF or GDNF-like molecules. Similar assays may involve neurturin and GRR2. In yet another embodiment, soluble GDNFR may be used to bind or detect the presence of GDNF or GDNF-like molecules.

30 In addition, the present invention provides for experimental model systems for studying the physiological role of GDNF or neurturin. Such systems include assays involving anti-GDNFR antibodies or oligonucleotide probes as well as animal models, such as transgenic animals which express high levels of GDNFR and therefore are hypersensitive to GDNF and/or neurturin or animals derived using embryonic stem cell technology in which the endogenous GDNFR genes were

deleted from the genome. An anti-GDNFR antibody will binds a peptide portion of the neurotrophic factor receptor proteins. Antibodies include monoclonal and polyclonal antibodies. Alternatively, immunological tags for which antibodies already exist may be attached to the GDNFR protein to aid in detection. Such tags
5 include but are not limited to Flag (IBI/Eastman Kodak) and myc sequences. Other tag sequences such as polyhistidine have also been used for detection and purification on metal chelating columns.

Yet another aspect of the present invention involves the use of GDNFRs to identify ligands which activate receptors as described in the following detailed
10 description and examples. Proteins as well as small molecule neurotrophic factor mimetics may be identified and studied following the binding studies described herein.

Additional aspects and advantages of the invention will be apparent to those skilled in the art upon consideration of the following description, which details the
15 practice of the present invention.

BRIEF DESCRIPTION OF THE FIGURES

20 Figure 1 depicts a nucleic acid sequence (SEQ ID NO:1) encoding human glial cell line-derived neurotrophic factor receptor (GDNFR- α). The amino acid sequence of the full length GDNFR protein is encoded by nucleic acids 540 to 1934.

Figure 2 depicts the amino acid sequence (SEQ ID NO:2) of the full length
25 human GDNFR- α protein.

Figure 3 depicts a nucleic acid sequence (SEQ ID NO:3) encoding rat GDNFR- α . The amino acid sequence of the full length GDNFR- α protein is encoded by nucleic acids 302 to 1705.

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Figure 4 depicts the amino acid sequence (SEQ ID NO:4) of the full length rat GDNFR- α protein

Figure 5 depicts the alignment and comparison of portions of GDNFR- α cDNA sequences produced in various clones as well as the consensus sequence for
35 human GDNFR- α .

Figure 6 depicts the identification of Neuro-2A derived cell lines expressing GDNFR- α .

Figure 7A and 7B depict the results of the equilibrium binding of
5 [125I]GDNF to cells expressing GDNFR- α .

Figure 8 depicts the results of the chemical cross-linking of [125I]GDNF to GDNFR- α and Ret Expressed in cells expressing GDNFR- α .

10 Figure 9 depicts the results of the induction of c-Ret autophosphorylation by GDNF in cells expressing GDNFR- α .

Figure 10 depicts the results of the induction of c-Ret autophosphorylation by GDNF and soluble GDNFR- α .

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Figure 11 depicts the results of the blocking of c-Ret autophosphorylation by a Ret-Fc fusion protein.

Figure 12 depicts the results of the induction of c-Ret autophosphorylation by
20 GDNF in motor neurons.

Figure 13 depicts a model for GDNF signaling mediated by GDNFR- α and Ret.

25 Figure 14 depicts a nucleic acid sequence (SEQ ID NO:__) encoding human glial cell line-derived neurotrophic factor receptor- α -related protein 2 (GRR2). The amino acid sequence of the full length GRR2 protein is encoded by nucleic acids 1585 to 2989.

30 Figure 15 depicts a nucleic acid sequence (SEQ ID NO:__) encoding human glial cell line-derived neurotrophic factor receptor- α -related protein 3 (GRR3).

Figure 16 depicts a nucleic acid sequence (SEQ ID NO:__) encoding rat glial cell line-derived neurotrophic factor receptor- α -related protein 2 (rat GRR2).

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Figure 17 depicts a nucleic acid sequence (SEQ ID NO:__) encoding rat glial cell line-derived neurotrophic factor receptor- α -related protein 3 (rat GRR3).

Figure 18 depicts the alignment and comparison of various human, rat and mouse GDNFR amino acid sequences.

5 Figure 19 depicts the alignment and comparison of human, rat and mouse GDNFR- α , GRR2 AND GRR3 amino acid sequences and an exemplary consensus GDNFR sequence.

10 Figure 20 depicts the alignment and comparison of human and rat GDNFR- α and GRR2 peptide sequences.

15 Figure 21 (Panels A and B) depicts the binding of neurturin and GDNF to LA-N-5 and NGR-38 cells. LA-N-5 (Panel A) and NGR-38 (Panel B) cells were incubated with 50 pM of either [125 I]NTN or [125 I]GDNF in the absence (light gray bars) or presence of unlabeled GDNF (dark gray bars) or neurturin (black bars) at 4°C for two hours.

20 Figure 22 depicts the results of the chemical cross-linking of neurturin and GDNF to GDNFR- α and GRR2.

Figure 23 depicts the results of neurturin induced *ret* autophosphorylation in NGR-38 cells.

25 Figure 24 depicts the results of neurturin induced *ret* autophosphorylation in LA-N-5 cells.

Figure 25 (Panels A and B) depicts the results of neurturin and GDNF induced MAP kinase activation in LA-N-5 and NGR-38 cells.

30 Figure 26 depicts the amino acid sequences of GDNFR- α , GRR2 and GRR3 are aligned and a consensus sequence is shown above the three receptor sequences. Upper case letters in the consensus sequence indicate amino acids that are conserve in all three receptors, lower case letters indicate that two of the three receptors share that amino acid, and dots indicate all three receptors have a different amino acid at that position. Predicted signal peptide sequences are underlined in GDNFR- α , GRR3; no signal peptide is predicted for GRR2. The hydrophobic C-terminal regions of all three putative receptors are underlined. Potential N-glycosylation

are shown in boldface and sites conserved between two receptors are outlined by boxes.

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DETAILED DESCRIPTION OF THE INVENTION

Glial cell line-derived neurotrophic factor (GDNF) is a potent neurotrophic factor which exhibits a broad spectrum of biological activities on a variety of cell types from both the central and peripheral nervous systems. It is a glycosylated, disulfide-linked dimer which is distantly related (less than 20% homology) to the transforming growth factor- β (TGF- β) superfamily. GDNF's ability to enhance the survival of dopaminergic neurons and other neuron populations demonstrates its therapeutic potential for the treatment of Parkinson's disease as well as other forms of nerve damage or malfunction.

The described biological activities of the neurturin neurotrophic factor (Nature 384(5):467-470, 1996) include promoting the survival of nodose ganglia sensory neurons and a small population of dorsal root ganglia sensory neurons, in addition to superior cervical ganglion sympathetic neurons. The activity suggests the possibility of a common or similar signaling pathway. In addition, the biological activities of neurturin may extend to motor neurons and dopaminergic neurons. Thus, neurturin may be useful in the treatment of diseases for which the use of GDNF may be indicated.

The present invention is based upon the discovery of a high affinity receptor first found on the surface of cultured retinal cells from postnatal rats. These receptors possess an estimated GDNF binding affinity comparable to that of the receptors found in dopaminergic and motor neurons; midbrain dopaminergic neurons (Lin et al., 1993 supra; Sauer et al., 1995 supra; Kearns and Gash, 1995 supra; Beck et al., 1995 supra; Tomac et al., 1995a supra), facial and spinal cord motor neurons (Li et al., 1995 supra; Oppenheim et al., 1995 supra; Yan et al., 1995 supra; Zurn et al., 1994 supra; Henderson et al., 1994 supra). The receptor molecule has been named GDNF receptor-alpha (GDNFR- α) since it is the first known component of a receptor system for GDNF. The present invention also provides the first description of the expression cloning and characterization of GDNFR- α protein. Cells modified to express the recombinant receptor bind GDNF with high affinity. Additional receptor proteins include glial cell line-derived neurotrophic factor receptor- α related receptor proteins 2 and 3 (GRR2 and GRR3).

Using a dopamine uptake assay and [125 I]-GDNF binding on cultured cells, high affinity receptors to GDNF were detected on the surface of rat photoreceptor cells. As further described in the Examples, the study of photoreceptor cells lead to the isolation of a cDNA clone by expression cloning for GDNFR- α . The nucleic acid sequence for GDNFR- α encodes a protein of 468 amino acids with 31 cysteine residues and three potential N-glycosylation sites. Next, a nucleic acid sequence from the rat cDNA clone was used to isolate its human homolog which was found to be nearly identical to the rat receptor at the amino acid level. The human GDNFR- α cDNA sequence encodes a protein of 465 amino acids with the positions of all cysteine residues and potential N-glycosylation sites conserved relative to the rat receptor. This high degree of primary sequence conservation indicated an important role for this receptor in the biological function of GDNF.

As discussed above, many receptors have three main domains: an extracellular or cell surface domain responsible for specifically binding a protein factor; a transmembrane domain which spans the cell's membrane; and an intracellular or cytoplasmic domain that is typically involved in initiating signal transduction when a protein factor binds to the extracellular domain. It was determined, however, that GDNFR- α is unrelated in sequence or structural characteristics to any known protein (such as the consensus sequences found in either receptor kinases or cytokine receptors), lacks a cytoplasmic domain, lacks the C-terminal charged residues characteristic of a transmembrane domain and is anchored to the cell membrane by glycosyl-phosphatidylinositol (GPI) linkage, as described in greater detail below. Although the absence of an intracellular catalytic domain precluded a direct role in transmembrane signaling, the high binding affinity and strong evolutionary sequence conservation further suggested that this receptor was important for GDNF function.

Because GDNFR- α lacks a cytoplasmic domain, it was thought that this receptor must act in conjunction with one or more accessory molecules which play a role in transmembrane signaling. It was then discovered that transgenic mice which lack the gene for GDNF die and have no kidneys. Transgenic mice which lack the gene for c-ret proto-oncogene (Schuchardt, et al., Nature, 367, 380-383, 1994) were found to have a similar phenotype. The c-ret proto-oncogene encodes a receptor tyrosine kinase (RTK) whose normal function had not yet been determined. All RTKs have a similar topology: they possess an extracellular ligand-binding domain, a transmembrane domain and a cytoplasmic segment containing the catalytic protein-tyrosine kinase domain. Binding of a ligand leads to the activation of the kinase domain and phosphorylation of specific substrates in the cell that mediate

intracellular signaling. The present invention involves the discovery that a soluble form of GDNFR- α may be used to mediate the binding of GDNF to the c-ret proto-oncogene and thereby elicit a cellular response to GDNF as well as modify its cell-type specificity.

5 Similar species, called "receptor alpha" components, provide ligand binding specificity but do not have the capacity to transduce signal on their own. Such components are found in the ciliary neurotrophic factor (CNTF) and interleukin-6 (IL-6) receptor systems. Like GDNFR- α , and in contrast to IL-6 receptor, CNTF receptor binds its ligand with high affinity, has a hydrophobic C-terminus, no
10 cytoplasmic domain, and is anchored to the cell membrane by GPI linkage (Davis et al., 1991). In order to mediate signal transduction, CNTF binds first to CNTF receptor, creating a complex which is able to bind gp130. This inactive complex then binds to LIF receptor to form the active signaling complex (Davis, et al., Science, 260, 1805-1807, 1993). As with the present invention, CNTF receptor (the
15 ligand specific binding component) must be present for signaling to occur but it need not be membrane bound (Economides et al., Science, 270, 1351-1353, 1995).

As further described below, the GDNFR protein may be anchored to a cell surface, or it may be provided in a soluble form. In either case, the GDNFR protein forms a ligand complex with GDNF and/or neurturin, and the ligand complex binds
20 to cell surface receptor to effectuate intracellular signaling. Thus, a soluble form of GDNFR protein may be used to potentiate the action of a neurotrophic factor that binds thereto and/or modify its cell-type specificity.

The GDNFR proteins are unrelated to previously known receptors. There are no apparent matches in the GenBank and Washington University-Merck databases
25 for related sequences. An expressed sequence tag (EST) found in the Washington University-Merck EST database shows 75% homology to a small portion of the coding region of GDNFR- α (approximately 340 nucleotides of the 521 nucleotides of sequence generated from the 5' end of the clone). This clone (GenBank accession #H12981) was isolated from an oligo-dT primed human infant brain library and
30 cloned directionally into the Lfmid BA vector (Hillier, L. et al, unpublished data). The 3' end of the #H12981 clone has been sequenced, but it exhibits no homology to any part of GDNFR- α . The appearance of homology between this #H12981 clone and GDNFR- α over a short region, which homology then disappears, suggests that the #H12981 clone represents an unspliced transcript, or cloning artifact rather than a
35 bona fide cDNA transcript.

Thus, the present invention enables the cloning of a GDNFR protein by providing a method for selecting target cells which express GDNFR protein. By

providing a means of enriching for GDNFR protein-encoding sequences, the present invention further provides for the purification of GDNFR protein and the direct cloning of GDNFR-encoding DNA. The present description of the GDNFR nucleic acid and amino acid sequences provides the information needed to reproduce these entities as well as a variety of GDNFR analogs. With this information, GDNFR protein products may be isolated or generated by any means known to those skilled in the art. A variety of means for the recombinant or synthetic production of GDNFR protein are disclosed.

As used herein, the term "GDNFR protein product" includes biologically active purified natural, synthetic or recombinant GDNFR- α , GRR2 and GRR3 (jointly referred to as glial cell line derived neurotrophic factor receptors, GDNFR, GDNFR protein), GDNFR analogs (i.e., GDNFR homologs and variants involving insertion, substitution and deletion variations, such as based on the consensus sequences depicted in the Figures), and chemically modified derivatives thereof. GDNFR analogs are substantially homologous to the GDNFR amino acid sequences set forth in the Figures.

The term "biologically active", as used herein, means that the GDNFR protein product demonstrates high affinity binding to GDNF and/or neurturin and mediates or enhances GDNF-induced or neurturin-induced signal transduction. Using the present disclosure, it is well within the ability of those of ordinary skill in the art to determine whether a GDNFR protein analog has substantially the same biological activity as the GDNFR protein products set forth in the Figures.

The term "substantially homologous" amino acid sequence, as used herein, refers to an amino acid sequence sharing a degree of "similarity" or homology to the GDNFR amino acid sequences set forth in the Figures such that the homologous sequence has a biological activity or function similar to that described for these GDNFR amino acid sequences. It will be appreciated by those skilled in the art, that a relatively large number of individual or grouped amino acid residues can be changed, positionally exchanged (e.g.s, reverse ordered or reordered) or deleted entirely in an amino acid sequence without affecting the three dimensional configuration or activity of the molecule. Such modifications are well within the ability of one skilled in the art following the present disclosure. The identification and means of providing such modified sequences are described in greater detail below. It is preferable that the degree of homology of a substantially homologous protein (peptide) is equal to or in excess of 70% (i.e., a range of from 70% to 100% homology). Thus, a preferable "substantially homologous" GDNFR amino acid sequence may have a degree of homology greater than or equal to 70% of the amino

acid sequences set forth for GDNFR- α , GRR2, GRR3 and consensus sequences thereof as depicted in the Figures. More preferably the degree of homology may be equal to or in excess of 80% or 85%. Even more preferably it is equal to or in excess of 90%, or most preferably it is equal to or in excess of 95%.

5 The percentage of homology as described herein is calculated as the percentage of amino acid residues found in one protein sequence which align with identical or similar amino acid residues in the second protein sequence. Thus, in the case of GDNFR protein homology, the degree of sequence homology may be determined by optimally aligning the amino acid residues of the comparison
10 molecule to those of a reference GDNFR polypeptide, such as depicted in the Figures or those encoded by the nucleic acid sequences depicted in the Figures, to maximize matches of residues between the two sequences. It will be appreciated by those skilled in the art that such alignment may include appropriate conservative residue substitutions and will disregard truncations and internal deletions or
15 insertions of the comparison sequence by introducing gaps as required; see, for example Dayhoff, Atlas of Protein Sequence and Structure Vol. 5, wherein an average of three or four gaps in a length of 100 amino acids may be introduced to assist in alignment (p. 124, National Biochemical Research Foundation, Washington, D.C., 1972; the disclosure of which is hereby incorporated by reference). Once so
20 aligned, the percentage is determined by the number of aligned residues in the comparison polypeptide divided by the total number of residues in the comparison polypeptide. It is further contemplated that the GDNFR protein sequences of the present invention may be used to form a portion of a fusion protein or chimeric protein which has, at least in part, GDNFR protein activity. The alignment and
25 homology of such a protein would be determined using that portion of the fusion protein or chimeric protein which is related to GDNFR protein activity.

 The sources of such substantially homologous GDNFR proteins include the GDNFR proteins of other mammals (such as depicted in the Figures) which are expected to have a high degree of homology to the human GDNFR protein. For
30 example, the degree of homology between the rat and human GDNFR- α proteins disclosed herein is about 93%. Substantially homologous GDNFR proteins may be isolated from such mammals by virtue of cross-reactivity with antibodies to the GDNFR amino acid sequences depicted in the Figures. Alternatively, they may be expressed by nucleic acid sequences which are isolated through hybridization with
35 the gene or with segments of the gene encoding the GDNFR proteins or which hybridize to a complementary sequence of the nucleic acid sequences illustrated in the Figures. Suitable hybridization conditions are described in further detail below.

The novel GDNFR protein products are typically isolated and purified to form GDNFR protein products which are substantially free of unwanted substances that would detract from the use of the present polypeptides for an intended purpose. For example, preferred GDNFR protein products may be substantially free from the presence of other human (e.g., non-GDNFR) proteinaceous materials or pathological agents. Preferably, the GDNFR protein products are about 80% free of other proteins which may be present due to the production technique used in the manufacture of the GDNFR protein product. More preferably, the GDNFR protein products are about 90% free of other proteins, particularly preferably, about 95% free of other proteins, and most preferably about >98% free of other proteins. In addition, the present invention furnishes the unique advantage of providing polynucleotide sequences for the manufacture of homogeneous GDNFR proteins.

A variety of GDNFR variants are contemplated, including addition, deletion and substitution variants. For example, a series of deletion variants may be made by removing one or more amino acid residues from the amino and/or carboxy termini of the GDNFR protein. Using rules for the prediction of signal peptide cleavage as described by von Heijne (von Heijne, *Nucleic Acids Research*, 14, 4683-4690, 1986), the first amino acid residue of the GDNFR- α protein which might be involved in GDNF binding is Ser¹⁸, as depicted in the full length amino acid sequence of human GDNFR- α in Figure 2 (SEQ ID NO:2). Amino acid residues Met¹ through Ser¹⁸ are in the amino-terminal hydrophobic region that is likely to be part of a signal peptide sequence, and therefore, not be included in the mature form of the receptor protein. Similarly, the last amino acid residue of the GDNFR- α protein which is likely to be necessary for GDNF binding is Ser⁴⁴⁶. Amino acid residues Leu⁴⁴⁷ through Ser⁴⁶⁵ are in the carboxy-terminal hydrophobic region that is involved in the GPI linkage of the protein to the cell surface. Thus, it is contemplated that any or all of the residues from Met¹ through Ser¹⁸ and/or Leu⁴⁴⁷ through Ser⁴⁶⁵ (as depicted in Figure 2 (SEQ ID NO:2)) may be removed from the protein without affecting GDNF binding to the GDNFR- α protein, thereby leaving a "core" sequence of Ala¹⁹ through Pro⁴⁴⁶. Using known analysis techniques, it is further contemplated that N-terminal truncations may include the removal of one or more amino acid residues up to and including Gly²⁴. Thus, GDNFR- α truncation analogs also may include the deletion of one or more amino acid residues from either or both termini such that an amino acid sequence of Asp²⁵ through Pro⁴⁴⁶ or Leu⁴⁴⁷ forms the basis for a core molecule. Additional GDNFR- α analogs are contemplated as involving amino acid residues Ser¹⁸ through Pro⁴⁴⁹ as depicted in the GDNFR- α amino acid sequence of Figure 4 (SEQ ID NO:4), i.e., deleting one or

more amino acid residues from either or both termini involving the hydrophobic regions depicted as amino acid residues Met¹ through Ser¹⁸ and/or Pro⁴⁴⁹ through Ser⁴⁶⁸. Similar analogs may be designed using the amino acid sequences for GRR2 and GRR3, as well as consensus sequences, as depicted in the Figures.

5 In addition, it is contemplated that one or more amino acid residues may be removed from either or both of the amino and carboxy termini of the GDNFR protein until the first and last cysteine residues in the full length sequence are reached. It is advantageous to retain the cysteine residues for the proper intramolecular binding of the GDNFR protein. As depicted in the full length amino acid sequence of human GDNFR- α in Figure 2 (SEQ ID NO:2), any or all of amino acid residues from Met¹ to Asp²⁸ may be removed from the amino terminal without removing the first cysteine residue which appears as Cys²⁹. Similarly, any or all of amino acid residues from Gly⁴⁴³ to Ser⁴⁶⁵ may be removed from the carboxy terminal without removing the last cysteine residue which appears as Cys⁴⁴². Other
10 GDNFR- α analogs may be made using amino acid residues Cys²⁹ through Cys⁴⁴³ as depicted in the GDNFR- α amino acid sequence of Figure 4 (SEQ ID NO:4), i.e., deleting all or part of the terminal regions depicted as amino acid residues Met¹ through Asp²⁸ and/or Ser⁴⁴⁴ through Ser⁴⁶⁸. Similar analogs may be designed using the amino acid sequences for GRR2 and GRR3, as well as consensus
15 sequences, as depicted in the Figures.

20 It will be appreciated by those skilled in the art that, for the same reasons, it is contemplated that these identified amino acid residues may be replaced, rather than deleted, without affecting the function of the GDNFR protein. Alternatively, these identified amino acid residues may be modified by intra-residue insertions or
25 terminal additions without affecting the function of the GDNFR protein. In yet another embodiment, a combination of one or more deletions, substitutions or additions may be made.

30 The present GDNFR proteins or nucleic acids may be used for methods of treatment, or for methods of manufacturing medicaments for treatment. Such treatment includes conditions characterized by excessive production of GDNF or neurturin, wherein the present GDNFRs, particularly in soluble form, may be used to complex to and therefore inactivate such excessive GDNF or neurturin. This treatment may be accomplished by preparing a soluble receptor (e.g., use of the
35 GDNF or neurturin binding domain) or by preparation of a population of cells containing such GDNFR, and transplanting such cells into the individual in need thereof. The present GDNFR protein products may also be used for treatment of

those having defective GDNF and/or neurturin receptors. For example, one may treat an individual having defective GDNFRs by preparation and delivery of a soluble receptor, or by preparation of a population of cells containing such non-defective GDNFR and transplanting such cells into an individual. Or, an individual
5 may have an inadequate number of GDNF or neurturin receptors, and cells containing such receptors may be transplanted in order to increase the number of GDNF or neurturin receptors available to an individual. Such compositions may be used in conjunction with the delivery of GDNF or neurturin. It is also contemplated GDNFR protein products may be used in the treatment of conditions responsive to
10 the activation of the c-ret receptor tyrosine kinase.

In yet another aspect of the present invention, a further advantage to the novel compositions is the use of GDNFR to stabilize GDNF protein or neurturin pharmaceutical compositions. In another aspect of the present invention, a GDNFR may be used to screen compounds for antagonist activity.

15 Other aspects and advantages of the present invention will be apparent to those skilled in the art. For example, additional uses include new assay systems, transgenic animals and antibody production.

Study Models

20 The present invention provides for assay systems in which GDNF or neurturin activity or activities similar to GDNF or neurturin activity resulting from exposure to a peptide or non-peptide compound may be detected by measuring an elicited physiological response in a cell or cell line which expresses the GDNFR molecules of the present invention. A physiological response may comprise any of
25 the biological effects of GDNF or neurturin, including but not limited to, dopamine uptake, extension of neurites, increased cell survival or growth, as well as the transcriptional activation of certain nucleic acid sequences (e.g. promoter/enhancer elements as well as structural genes), GDNF-related processing, translation, or phosphorylation, and the induction of secondary processes in response to processes
30 directly or indirectly induced by GDNF, to name but a few.

For example, a model system may be created which may be used to study the effects of excess GDNF activity. In such a system, the response of a cell to GDNF may be increased by engineering an increased number of suitable GDNFRs on the cells of the model system relative to cells which have not been so modified. A
35 system may also be developed to selectively provide an increased number of such GDNFRs on cells which normally express GDNFRs. In order to ensure expression of GDNFR, the GDNFR gene may be placed under the control of a suitable promoter

sequence. It may be desirable to put the GDNFR gene under the control of a constitutive and/or tissue specific promoter (including but not limited to the CNS neuron specific enolase, neurofilament, and tyrosine hydroxylase promoter), an inducible promoter (such as the metallothionein promoter), the UV activated promoter in the human immunodeficiency virus long terminal repeat (Valeri et al., 1988, Nature 333:78-81), or the CMV promoter (as contained in pCMX, infra) or a developmentally regulated promoter.

By increasing the number of cellular GDNFRs, the response to endogenous GDNF may be increased. If the model system contains little or no GDNF, GDNF may be added to the system. It may also be desirable to add additional GDNF to the model system in order to evaluate the effects of excess GDNF activity. Over expressing GDNF (or secreted GDNF) may be one method for studying the effects of elevated levels of GDNF on cells already expressing GDNFR.

GDNFR Therapies

In another aspect, certain conditions may benefit from an increase in GDNF and/or neurturin responsiveness. It may, therefore, be beneficial to increase the number or binding affinity of GDNFRs in patients suffering from conditions responsive to GDNF and/or neurturin therapy. This could be achieved through gene therapy, whereby selective expression of recombinant GDNFR in appropriate cells is achieved, for example, by using GDNFR genes controlled by tissue specific or inducible promoters or by producing localized infection with replication defective viruses carrying a recombinant GDNFR gene.

It is envisioned that conditions which will benefit from GDNFR or combined GDNF or neurturin/GDNFR delivery include, but are not limited to, motor neuron disorders including amyotrophic lateral sclerosis, neurological disorders associated with diabetes, Parkinson's disease, Alzheimer's disease, and Huntington's chorea. Additional indications for the use of GDNFR or combined GDNF or neurturin/GDNFR delivery are described above and further include the treatment of: glaucoma or other diseases and conditions involving retinal ganglion cell degeneration; sensory neuropathy caused by injury to, insults to, or degeneration of, sensory neurons; pathological conditions, such as inherited retinal disease, age, disease or injury-related retinopathies, in which photoreceptor degeneration occurs and is responsible for vision loss; and injury or degeneration of sensory cells, such as hair cells and auditory neurons for preventing hearing loss due to variety of causes.

Transgenic Animals

In yet another aspect, a recombinant GDNFR gene may be used to inactivate or "knock out" the endogenous gene (e.g., by homologous recombination) and thereby create a GDNFR deficient cell, tissue, or animal. For example, a recombinant GDNFR- α gene may be engineered to contain an insertional mutation which inactivates GDNFR- α . Such a construct, under the control of a suitable promoter, may be introduced into a cell, such as an embryonic stem cell, by any conventional technique including transfection, transduction, injection, etc. Cells containing the construct may then be selected, for example by G418 resistance. Cells which lack an intact GDNFR- α gene are then identified (e. g., by Southern blotting or Northern blotting or assay of expression). Cells lacking an intact GDNFR- α gene may then be fused to early embryo cells to generate transgenic animals deficient in GDNFR. A comparison of such an animal with an animal not expressing endogenous GDNF would reveal that either the two phenotypes match completely or that they do not, implying the presence of additional GDNF-like factors or receptors. Such an animal may be used to define specific neuronal populations, or other in vivo processes, normally dependent upon GDNF. Thus, these populations or processes may be expected to be effected if the animal did not express GDNFR- α , and therefore, could not respond to GDNF. Similar constructs may be made and procedures followed for GRR2 and GRR3.

Diagnostic Applications

According to the present invention, GDNFR probes may be used to identify cells and tissues which are responsive to GDNF or neurturin in normal or diseased states. The present invention provides for methods for identifying cells which are responsive to GDNF or neurturin by detecting GDNFR expression in such cells. GDNFR expression may be evidenced by transcription of GDNFR mRNA or production of GDNFR protein. GDNFR expression may be detected using probes which identify GDNFR nucleic acid or protein or by detecting "tag" sequences artificially added to the GDNFR protein.

One variety of probe which may be used to detect GDNFR expression is a nucleic acid probe, which may be used to detect GDNFR-encoding RNA by any method known in the art, including, but not limited to, in situ hybridization, Northern blot analysis, or PCR related techniques. Nucleic acid products of the invention may be labeled with detectable markers (such as radiolabels and non-isotopic labels such as biotin) and employed in hybridization processes to locate the human GDNFR gene position and/or the position of any related gene family in a

chromosomal map. They may also be used for identifying human GDNFR gene disorders at the DNA level and used as gene markers for identifying neighboring genes and their disorders. Contemplated herein are kits containing such labeled materials.

5 Polypeptide products of the invention may be "labeled" by association with a detectable marker substance or label (e.g., a radioactive isotope, a fluorescent or chemiluminescent chemical, an enzyme or other label available to one skilled in the art) to provide reagents useful in detection and quantification of GDNF or neurturin in solid tissue and fluid samples such as blood or urine. Such products may also be
10 used in detecting cells and tissues which are responsive to GDNF or neurturin in normal or diseased states.

Another possible assay for detecting the presence of GDNF or neurturin in a test sample or screening for the presence of a GDNF-like molecule involves contacting the test sample with a GDNFR protein, suitable for binding GDNF or
15 neurturin, immobilized on a solid phase, thereby producing GDNFR-bound GDNF or neurturin protein. The GDNFR-bound GDNF or neurturin may optionally be contacted with a detection reagent, such as a labeled antibody specific for GDNF or neurturin, thereby forming a detectable product. Such assays may be developed in the form of assay devices for analyzing a test sample. In a basic form, such devices
20 include a solid phase containing or coated with an appropriate GDNFR protein. A method for analyzing a test sample for the presence of GDNF-like protein may involve contacting the sample to an assay reagent comprising GDNFR protein, wherein said GDNFR protein reacts with the GDNF-like protein present in the test sample and produces a detectable reaction product indicative of the presence of
25 GDNF.

The assay reagents provided herein may also be embodied as part of a kit or article of manufacture. Contemplated is an article of manufacture comprising a packaging material and one or more preparations of the presently provided nucleic acid or amino acid sequences. Such packaging material will comprise a label
30 indicating that the preparation is useful for detecting GDNF, neurturin, GDNFR or GDNFR defects in a biological sample. As such, the kit may optionally include materials to carry out such testing, such as reagents useful for performing protein analysis, DNA or RNA hybridization analysis, or PCR analysis on blood, urine, or tissue samples.

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Anti-GDNFR Antibody

According to the present invention, GDNFR protein, or fragments or

derivatives thereof, may be used as an immunogen to generate anti-GDNFR antibodies. To further improve the likelihood of producing an anti-GDNFR immune response, the amino acid sequence of GDNFR may be analyzed in order to identify portions of the molecule which may be associated with increased immunogenicity.

- 5 For example, the amino acid sequence may be subjected to computer analysis to identify surface epitopes which present computer-generated plots of hydrophilicity, surface probability, flexibility, antigenic index, amphiphilic helix, amphiphilic sheet, and secondary structure of GDNFR. Alternatively, the amino acid sequences of GDNFR from different species could be compared, and relatively non-homologous regions identified; these non-homologous regions would be more likely to be immunogenic across various species.

Also comprehended are polypeptide fragments duplicating only a part of the continuous amino acid sequence or secondary conformations within GDNFR, which fragments may possess one activity of mammalian GDNFR (e.g., immunological activity) and not others (e.g., GDNF protein binding activity). Thus, the production of antibodies can include the production of anti-peptide antibodies. The following exemplary peptides were synthesized using GDNFR sequences:

Table 1

GDNFR- α Peptides

SJP-6	H ₂ N-QSCSTKYRTL-COOH	human GDNFR- α , AA 40-49 (SEQ ID NO:25)
SJP-7	H ₂ N-CKRGMKKEKN-COOH	human GDNFR- α , AA 89-98 (SEQ ID NO:26)
SJP-8	H ₂ N-LLEDSPYEPV-COOH	human GDNFR- α , AA 115-124 (SEQ ID NO:27)
SJP-9	H ₂ N-CSYEERERPN-COOH	rat GDNFR- α , AA 233-242 (SEQ ID NO:28)
SJP-10	H ₂ N-PAPPVQTTTATTTT-COOH	rat GDNFR- α , AA 356-369 (SEQ ID NO:29)

Peptides SJP-6, 7, and 8 are identical in rat and human GDNFR- α . Peptides SJP-9 and 10 are derived from the rat sequence and are each one amino acid different from human. Both polyclonal and monoclonal antibodies may be made by methods known in the art using these peptides or other portions of GDNFR.

Monoclonal antibodies directed against GDNFR may be prepared by any known technique which provides for the production of antibody molecules by continuous cell lines in culture. For example, the hybridoma technique originally developed by Kohler and Milstein to produce monoclonal antibodies (Nature, 256:495-497, 1975), as well as the trioma technique, the human B-cell hybridoma technique (Kozbor et al., Immunology Today 4:72, 1983), the EBV-hybridoma

technique (Cole et al., in "Monoclonal Antibodies and Cancer Therapy," Alan R. Liss, Inc. pp. 77-96, 1985), and the like, may be used.

Human monoclonal antibodies or chimeric human-mouse (or other species) monoclonal antibodies also may be prepared for therapeutic use and may be made by
5 any of numerous techniques known in the art (e.g., Teng et al., Proc. Natl. Acad. Sci. U.S.A., 80:7308-7312, 1983; Kozbor et al., Immunology Today, 4:72-79, 1983; Olsson et al., Meth. Enzymol., 92:3-16, 1982). Chimeric antibody molecules may be prepared containing a mouse antigen-binding domain with human constant regions (Morrison et al., Proc. Natl. Acad. Sci. U.S.A., 81:6851, 1984; Takeda et al., Nature,
10 314:452, 1985).

Various procedures known in the art also may be used for the production of polyclonal antibodies. For the production of antibody, various host animals including, but not limited to, rabbits, mice, rats, etc., can be immunized by injection with GDNFR protein, or a fragment or derivative thereof. Various adjuvants may be
15 used to increase the immunological response, depending on the host species selected. Useful adjuvants include, but are not limited to, Freund's (complete and incomplete), mineral gels such as aluminum hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanins, dinitrophenol, and human adjuvants such as BCG (Bacille Calmette-
20 Guerin) and Corynebacterium parvum.

A molecular clone of an antibody to a GDNFR epitope also may be prepared by known techniques. Recombinant DNA methodology (see e.g., Maniatis et al., Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y., 1982) may be used to construct nucleic acid sequences which
25 encode a monoclonal antibody molecule, or antigen binding region thereof.

Antibody molecules may be purified by known techniques, e.g., immunoabsorption or immunoaffinity chromatography, chromatographic methods such as high performance liquid chromatography, or a combination thereof, etc. The present invention provides for antibody molecules as well as fragments of such
30 antibody molecules. Antibody fragments which contain the idiotype of the molecule can be generated by known techniques. For example, such fragments include but are not limited to: the F(ab')₂ fragment which can be produced by pepsin digestion of the antibody molecule; the Fab' fragments which can be generated by reducing the disulfide bridges of the F(ab')₂ fragment, and the Fab fragments which can be
35 generated by treating the antibody molecule with papain and a reducing agent.

Such selective binding molecules may themselves be alternatives to GDNFR protein, and may be formulated as a pharmaceutical composition.

Recombinant Expression of GDNFR Protein

The present invention provides various polynucleotides encoding GDNFR proteins. The expression product or a derivative thereof is characterized by the ability to bind to GDNF or neurturin so that further interactions with signaling molecules can occur, thereby providing or enhancing GDNF or neurturin activity such as increasing dopamine uptake by dopaminergic cells. The polynucleotides may also be used in cell therapy or gene therapy applications.

According to the present invention, novel GDNFR protein and DNA sequences coding for all or part of such receptors are provided. Novel nucleic acid sequences of the invention are useful in securing expression in procaryotic or eucaryotic host cells of polypeptide products having at least a part of the primary structural conformation and one or more of the biological properties of recombinant human GDNFR. The nucleic acids may be purified and isolated, so that the desired coding region is useful to produce the present polypeptides. Alternatively, the nucleic acid sequence may be used for diagnostic purposes, as described more fully below. Exemplary DNA sequences of the present invention comprise nucleic acid sequences encoding the GDNFR- α amino acid sequences depicted in Figures 2 and 4 and set forth in SEQ. ID NOs:2 and 4. In addition, DNA sequences disclosed by the present invention include: (a) the GDNFR DNA sequences depicted in the Figures (and complementary strands); (b) a DNA sequence which hybridizes (under hybridization conditions disclosed in the cDNA library screening section below, or equivalent conditions or more stringent conditions) to the DNA sequence in subpart (a) or to fragments thereof; and (c) a DNA sequence which, but for the degeneracy of the genetic code, would hybridize to the DNA sequence in subpart (a). Specifically comprehended in parts (b) and (c) are genomic DNA sequences encoding allelic variant forms of human GDNFR and/or encoding GDNFR from other mammalian species, and manufactured DNA sequences encoding GDNFR, fragments of GDNFR, and analogs of GDNFR which DNA sequences may incorporate codons facilitating transcription and translation of messenger RNA in microbial hosts. Such manufactured sequences may readily be constructed according to the methods known in the art as well as the methods described herein.

Recombinant expression techniques, conducted in accordance with the descriptions set forth herein or other known methods, may be used to produce these polynucleotides and express the various GDNFR proteins. For example, by inserting a nucleic acid sequence which encodes a GDNFR protein into an appropriate vector, one skilled in the art can readily produce large quantities of the desired nucleotide

sequence. The sequences can then be used to generate detection probes or amplification primers. Alternatively, a polynucleotide encoding a GDNFR protein can be inserted into an expression vector. By introducing the expression vector into an appropriate host, the desired GDNFR protein may be produced in large amounts.

5 As further described herein, there are numerous host/vector systems available for the propagation of nucleic acid sequences and/or the production of GDNFR proteins. These include, but are not limited to, plasmid, viral and insertional vectors, and prokaryotic and eukaryotic hosts. One skilled in the art can adapt a host/vector system which is capable of propagating or expressing heterologous DNA to produce
10 or express the sequences of the present invention.

By means of such recombinant techniques, the GDNFR proteins of the present invention are readily produced in commercial quantities with greater purity. Furthermore, it will be appreciated by those skilled in the art that, in view of the present disclosure, the novel nucleic acid sequences include degenerate nucleic acid
15 sequences encoding the GDNFR proteins specifically set forth in the Figures, sequences encoding variants of GDNFR proteins, and those nucleic acid sequences which hybridize, preferably under stringent hybridization conditions, to complements of these nucleic acid sequences (see, Maniatis et. al., Molecular Cloning (A Laboratory Manual); Cold Spring Harbor Laboratory, pages 387 to 389,
20 1982.) Exemplary stringent hybridization conditions are hybridization in 4 x SSC at 62-67°C, followed by washing in 0.1 x SSC at 62-67°C for approximately an hour. Alternatively, exemplary stringent hybridization conditions are hybridization in 45-55% formamide, 4 x SSC at 40-45°C. DNA sequences which hybridize to the complementary sequences for GDNFR protein under relaxed hybridization
25 conditions and which encode a GDNFR protein of the present invention are also included herein. Examples of such relaxed stringency hybridization conditions are 4 x SSC at 45-55°C or hybridization with 30-40% formamide at 40-45°C.

Preparation of Polynucleotides Encoding GDNFR

30 Based upon the disclosure of the present invention, a nucleic acid sequence encoding a full length GDNFR protein or a fragment thereof may readily be prepared or obtained by a variety of means, including, without limitation, chemical synthesis, cDNA or genomic library screening, expression library screening, and/or PCR amplification of cDNA. These methods and others useful for preparing nucleic acid
35 sequences are known in the art and are set forth, for example, by Sambrook et al. (Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989), by Ausubel et al., eds (Current Protocols in

Molecular Biology, Current Protocols Press, 1994), and by Berger and Kimmel (Methods in Enzymology: Guide to Molecular Cloning Techniques, vol. 152, Academic Press, Inc., San Diego, CA, 1987). Preferred nucleic acid sequences encoding GDNFR are mammalian sequences.

5 Chemical synthesis of a nucleic acid sequence which encodes a GDNFR protein can also be accomplished using methods known in the art, such as those set forth by Engels et al. (Angew. Chem. Intl. Ed., 28:716-734, 1989). These methods include, inter alia, the phosphotriester, phosphoramidite and H-phosphonate methods of nucleic acid sequence synthesis. A preferred method for such chemical synthesis
10 is polymer-supported synthesis using standard phosphoramidite chemistry. Typically, the DNA encoding the desired polypeptide will be several hundred base pairs (bp) or nucleotides in length. Nucleic acid sequences larger than about 100 nucleotides can be synthesized as several fragments using these methods. The fragments can then be ligated together to form a sequence for the expression of a full
15 length GDNFR protein or a portion thereof.

 Alternatively, a suitable nucleic acid sequence may be obtained by screening an appropriate cDNA library (i.e., a library prepared from one or more tissue source(s) believed to express the protein) or a genomic library (a library prepared from total genomic DNA). The source of the cDNA library is typically a tissue that
20 is believed to express GDNFR in reasonable quantities. Typically, the source of the genomic library is any tissue or tissues from a mammalian species believed to harbor a gene encoding GDNFR. The library can be screened for the presence of the GDNFR cDNA/gene using one or more nucleic acid probes (such as oligonucleotides, cDNA or genomic DNA fragments based upon the presently
25 disclosed sequences) that will hybridize selectively with GDNFR cDNA(s) or gene(s) present in the library. The probes typically used for such library screening usually encode a small region of the GDNFR nucleic acid sequence from the same or a similar species as the species from which the library was prepared. Alternatively, the probes may be degenerate, as discussed herein.

30 Library screening is typically accomplished by annealing the oligonucleotide probe or cDNA to the clones in the library under conditions of stringency that prevent non-specific binding but permit binding (hybridization) of those clones that have a significant level of homology with the probe or primer. Typical hybridization and washing stringency conditions depend in part on the size (i.e., number of
35 nucleotides in length) of the cDNA or oligonucleotide probe, and whether the probe is degenerate. The probability of obtaining a clone(s) is also considered in designing the hybridization solution (e.g., whether a cDNA or genomic library is being

screened; if it is a cDNA library, the probability that the cDNA of interest is present at a high level).

Where DNA fragments (such as cDNAs) are used as probes, typical hybridization conditions include those as set forth in Ausubel et al., eds., supra.

5 After hybridization, the blot containing the library is washed at a suitable stringency, depending on several factors such as probe size, expected homology of probe to clone, type of library being screened, number of clones being screened, and the like. Examples of stringent washing solutions (which are usually low in ionic strength and are used at relatively high temperatures) are as follows. One such stringent wash is
10 0.015 M NaCl, 0.005 M NaCitrate and 0.1% SDS at 55-65°C. Another such stringent buffer is 1 mM Na₂EDTA, 40 mM NaHPO₄, pH 7.2, and 1% SDS at about 40-50°C. One other stringent wash is 0.2 X SSC and 0.1% SDS at about 50-65°C.

There are also exemplary protocols for stringent washing conditions where oligonucleotide probes are used to screen cDNA or genomic libraries. For example,
15 a first protocol uses 6 X SSC with 0.05 percent sodium pyrophosphate at a temperature of between about 35 and 62°C, depending on the length of the probe. For example, 14 base probes are washed at 35-40°C, 17 base probes at 45-50°C, 20 base probes at 52-57°C, and 23 base probes at 57-63°C. The temperature can be increased 2-3°C where the background non-specific binding appears high. A second
20 protocol uses tetramethylammonium chloride (TMAC) for washing. One such stringent washing solution is 3 M TMAC, 50 mM Tris-HCl, pH 8.0, and 0.2% SDS.

Another suitable method for obtaining a nucleic acid sequence encoding a GDNFR protein is by polymerase chain reaction (PCR). In this method, poly(A)+RNA or total RNA is extracted from a tissue that expresses GDNFR. A
25 cDNA is then prepared from the RNA using the enzyme reverse transcriptase (i.e., RT-PCR). Two primers, typically complementary to two separate regions of the GDNFR cDNA (oligonucleotides), are then added to the cDNA along with a polymerase such as Taq polymerase, and the polymerase amplifies the cDNA region between the two primers.

30 Where the method of choice for preparing the nucleic acid sequence encoding the desired GDNFR protein requires the use of oligonucleotide primers or probes (e.g., PCR, cDNA or genomic library screening), the oligonucleotide sequences selected as probes or primers should be of adequate length and sufficiently unambiguous so as to minimize the amount of non-specific binding that will occur
35 during library screening or PCR amplification. The actual sequence of the probes or primers is usually based on conserved or highly homologous sequences or regions from the same or a similar gene from another organism, such as the rat nucleic acid

sequence involved in the present invention. Optionally, the probes or primers can be fully or partially degenerate, i.e., contain a mixture of probes/primers, all encoding the same amino acid sequence, but using different codons to do so. An alternative to preparing degenerate probes is to place an inosine in some or all of those codon positions that vary by species. The oligonucleotide probes or primers may be prepared by chemical synthesis methods for DNA as described above.

GDNFR proteins based on these nucleic acid sequences encoding GDNFR, as well as mutant or variant sequences thereof, are also contemplated as within the scope of the present invention. Mutant or variant sequences include those sequences containing one or more nucleotide substitutions, deletions, and/or insertions as compared to the wild type sequence and that results in the expression of amino acid sequence variations as compared to the wild type amino acid sequence. In some cases, naturally occurring GDNFR amino acid mutants or variants may exist, due to the existence of natural allelic variation. GDNFR proteins based on such naturally occurring mutants or variants are also within the scope of the present invention. Preparation of synthetic mutant sequences is also well known in the art, and is described for example in Wells et al. (Gene, 34:315, 1985) and in Sambrook et al., *supra*.

In some cases, it may be desirable to prepare nucleic acid and/or amino acid variants of naturally occurring GDNFR. Nucleic acid variants (wherein one or more nucleotides are designed to differ from the wild-type or naturally occurring GDNFR) may be produced using site directed mutagenesis or PCR amplification where the primer(s) have the desired point mutations (see Sambrook et al., *supra*, and Ausubel et al., *supra*, for descriptions of mutagenesis techniques). Chemical synthesis using methods described by Engels et al., *supra*, may also be used to prepare such variants. Other methods known to the skilled artisan may be used as well. Preferred nucleic acid variants are those containing nucleotide substitutions accounting for codon preference in the host cell that is to be used to recombinantly produce GDNFR. Other preferred variants are those encoding conservative amino acid changes (e.g., wherein the charge or polarity of the naturally occurring amino acid side chain is not altered substantially by substitution with a different amino acid) as compared to wild type, and/or those designed to either generate a novel glycosylation and/or phosphorylation site(s) on GDNFR, or those designed to delete an existing glycosylation and/or phosphorylation site(s) on GDNFR. Yet other preferred variants are those encoding a GDNFR based upon a GDNFR consensus sequence as depicted in the Figures.

Vectors

The cDNA or genomic DNA encoding the desired GDNFR protein is inserted into a vector for further cloning (amplification of the DNA) or for expression. Suitable vectors are commercially available, or the vector may be specially constructed. Possible vectors include, but are not limited to, cosmids, plasmids or modified viruses, but the vector system must be compatible with the selected host cell. Such vectors include, but are not limited to, bacteriophages such as lambda derivatives, or plasmids such as pBR322, pUC, or Bluescript® plasmid derivatives (Stratagene, La Jolla CA). The recombinant molecules can be introduced into host cells via transformation, transfection, infection, electroporation, or other known techniques.

For example, the GDNFR-encoding nucleic acid sequence is inserted into a cloning vector which is used to transform, transfect, or infect appropriate host cells so that many copies of the nucleic acid sequence are generated. This can be accomplished by ligating a DNA fragment into a cloning vector which has complementary cohesive termini. If the complementary restriction sites used to fragment the DNA are not present in the cloning vector, the ends of the DNA molecules may be enzymatically modified. It also may prove advantageous to incorporate restriction endonuclease cleavage sites into the oligonucleotide primers used in polymerase chain reaction to facilitate insertion of the resulting nucleic acid sequence into vectors. Alternatively, any site desired may be produced by ligating nucleotide sequences (linkers) onto the DNA termini; these ligated linkers may comprise specific chemically synthesized oligonucleotides encoding restriction endonuclease recognition sequences. In an alternative method, the cleaved vector and GDNFR-encoding nucleic acid sequence may be modified by homopolymeric tailing. In specific embodiments, transformation of host cells with recombinant DNA molecules that incorporate an isolated GDNFR gene, cDNA, or synthesized DNA sequence enables generation of multiple copies of the gene. Thus, the GDNFR-encoding nucleic acid sequence may be obtained in large quantities by growing transformants, isolating the recombinant DNA molecules from the transformants and, when necessary, retrieving the inserted gene from the isolated recombinant DNA.

The selection or construction of the appropriate vector will depend on 1) whether it is to be used for DNA amplification or for DNA expression, 2) the size of the DNA to be inserted into the vector, and 3) the host cell (e.g., mammalian, insect, yeast, fungal, plant or bacterial cells) to be transformed with the vector. Each vector contains various components depending on its function (amplification of DNA or

expression of DNA) and its compatibility with the intended host cell. For DNA expression, the vector components may include, but are not limited to, one or more of the following: a signal sequence, an origin of replication, one or more selection or marker genes, enhancer elements, promoters, a transcription termination sequence, and the like. These components may be obtained from natural sources or synthesized by known procedures. The vectors of the present invention involve a nucleic acid sequence which encodes the GDNFR protein of interest operatively linked to one or more amplification, expression control, regulatory or similar operational elements capable of directing, controlling or otherwise effecting the amplification or expression of the GDNFR-encoding nucleic acid sequence in the selected host cell.

Expression vectors containing GDNFR nucleic acid sequence inserts can be identified by three general approaches: (a) DNA-DNA hybridization; (b) the presence or absence of "marker" gene functions, and (c) the expression of inserted sequences. In the first approach, the presence of a foreign nucleic acid sequence inserted in an expression vector can be detected by DNA-DNA hybridization using probes comprising sequences that are homologous to an inserted GDNFR-encoding nucleic acid sequence. In the second approach, the recombinant vector/host system can be identified and selected based upon the presence or absence of certain "marker" gene functions (e.g., thymidine kinase activity, resistance to antibiotics, transformation phenotype, occlusion body formation in baculovirus, etc.) caused by the insertion of a foreign nucleic acid sequence into the vector. For example, if a GDNFR-encoding nucleic acid sequence is inserted within the marker gene sequence of the vector, recombinants containing the GDNFR insert can be identified by the absence of the marker gene function. In the third approach, recombinant expression vectors can be identified by detecting the foreign protein product expressed by the recombinant nucleic acid sequence. Such assays can be based on the physical or functional properties of the expressed GDNFR protein product, for example, by binding of the GDNFR- α protein to GDNF or to an antibody which directly recognizes GDNFR- α .

Signal Sequence

The signal sequence may be a component of the vector, or it may be a part of GDNFR DNA that is inserted into the vector. The native GDNFR DNA encodes a signal sequence at the amino terminus of the protein that is cleaved during post-translational processing of the protein to form the mature GDNFR protein. Included within the scope of this invention are GDNFR polynucleotides with the native signal

sequence as well as GDNFR polynucleotides wherein the native signal sequence is deleted and replaced with a heterologous signal sequence. The heterologous signal sequence selected should be one that is recognized and processed, i.e., cleaved by a signal peptidase, by the host cell. For prokaryotic host cells that do not recognize and process the native GDNFR signal sequence, the signal sequence is substituted by a prokaryotic signal sequence selected, for example, from the group of the alkaline phosphatase, penicillinase, or heat-stable enterotoxin II leaders. For yeast secretion, the native GDNFR signal sequence may be substituted by the yeast invertase, alpha factor, or acid phosphatase leaders. In mammalian cell expression the native signal sequence is satisfactory, although other mammalian signal sequences may be suitable.

Origin of Replication

Expression and cloning vectors generally include a nucleic acid sequence that enables the vector to replicate in one or more selected host cells. In cloning vectors, this sequence is typically one that enables the vector to replicate independently of the host chromosomal DNA, and includes origins of replication or autonomously replicating sequences. Such sequences are well known for a variety of bacteria, yeasts, and viruses. The origin of replication from the plasmid pBR322 is suitable for most Gram-negative bacteria and various origins (e.g., SV40, polyoma, adenovirus, VSV or BPV) are useful for cloning vectors in mammalian cells. Generally, the origin of replication component is not needed for mammalian expression vectors (for example, the SV40 origin is often used only because it contains the early promoter).

Selection Gene

The expression and cloning vectors may contain a selection gene. This gene encodes a "marker" protein necessary for the survival or growth of the transformed host cells when grown in a selective culture medium. Host cells that were not transformed with the vector will not contain the selection gene, and therefore, they will not survive in the culture medium. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, e.g., ampicillin, neomycin, methotrexate, or tetracycline; (b) complement auxotrophic deficiencies; or (c) supply critical nutrients not available from the culture medium.

Other selection genes may be used to amplify the gene which will be expressed. Amplification is the process wherein genes which are in greater demand for the production of a protein critical for growth are reiterated in tandem within the

chromosomes of successive generations of recombinant cells. Examples of suitable selectable markers for mammalian cells include dihydrofolate reductase (DHFR) and thymidine kinase. The mammalian cell transformants are placed under selection pressure which only the transformants are uniquely adapted to survive by virtue of the marker present in the vector. Selection pressure is imposed by culturing the transformed cells under conditions in which the concentration of selection agent in the medium is successively changed, thereby leading to amplification of both the selection gene and the DNA that encodes GDNFR. As a result, increased quantities of GDNFR are synthesized from the amplified DNA.

For example, cells transformed with the DHFR selection gene are first identified by culturing all of the transformants in a culture medium that contains methotrexate, a competitive antagonist of DHFR. An appropriate host cell when wild-type DHFR is used is the Chinese hamster ovary cell line deficient in DHFR activity (see, for example, Urlaub and Chasin, Proc. Natl. Acad. Sci., U.S.A., 77(7): 4216-4220, 1980). The transformed cells are then exposed to increased levels of methotrexate. This leads to the synthesis of multiple copies of the DHFR gene, and, concomitantly, multiple copies of other DNA present in the expression vector, such as the DNA encoding a GDNFR protein.

Promoter

The expression and cloning vectors of the present invention will typically contain a promoter that is recognized by the host organism and operably linked to the nucleic acid sequence encoding the GDNFR protein. Promoters are untranslated sequences located upstream (5') to the start codon of a structural gene (generally within about 100 to 1000 bp) that control the transcription and translation of a particular nucleic acid sequence, such as that encoding GDNFR. Promoters are conventionally grouped into one of two classes, inducible promoters and constitutive promoters. Inducible promoters initiate increased levels of transcription from DNA under their control in response to some change in culture conditions, such as the presence or absence of a nutrient or a change in temperature. A large number of promoters, recognized by a variety of potential host cells, are well known. These promoters are operably linked to the DNA encoding GDNFR by removing the promoter from the source DNA by restriction enzyme digestion and inserting the desired promoter sequence into the vector. The native GDNFR promoter sequence may be used to direct amplification and/or expression of GDNFR DNA. A heterologous promoter is preferred, however, if it permits greater transcription and higher yields of the expressed protein as compared to the native promoter, and if it is

compatible with the host cell system that has been selected for use.

Promoters suitable for use with prokaryotic hosts include the beta-lactamase and lactose promoter systems; alkaline phosphatase, a tryptophan (trp) promoter system; and hybrid promoters such as the tac promoter. Other known bacterial
5 promoters are also suitable. Their nucleotide sequences have been published, thereby enabling one skilled in the art to ligate them to the desired DNA sequence(s), using linkers or adaptors as needed to supply any required restriction sites.

Suitable promoting sequences for use with yeast hosts are also well known in the art. Yeast enhancers are advantageously used with yeast promoters. Suitable
10 promoters for use with mammalian host cells are well known and include those obtained from the genomes of viruses such as polyoma virus, fowlpox virus, adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus and most preferably Simian Virus 40 (SV40). Other suitable mammalian promoters include heterologous mammalian
15 promoters, e.g., heat-shock promoters and the actin promoter. A promoter for possible use in the production of GDNFR proteins in CHO cells is SRa (see Takebe et al., Mol. Cell. Biol., 8(1): 466-472, 1988). A suitable expression vector is pDSRa2. The pDSRa2 plasmid constructs containing the appropriate GDNFR cDNA may be prepared substantially in accordance with the process described in the
20 co-owned and copending U. S. Patent Application Serial Number 501,904 filed March 29, 1990 (also see, European Patent Application No. 90305433, Publication No. EP 398 753, filed May 18, 1990 and WO 90/14363 (1990), the disclosures of which are hereby incorporated by reference.

Additional promoters which may be of interest in controlling GDNFR
25 expression include, but are not limited to: the SV40 early promoter region (Bernoist and Chambon, Nature, 290:304-310, 1981); the CMV promoter; the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto, et al., Cell, 22:787-797, 1980); the herpes thymidine kinase promoter (Wagner et al., Proc. Natl. Acad. Sci. U.S.A., 78:144-1445, 1981); the regulatory sequences of the
30 metallothioneine gene (Brinster et al., Nature, 296:39-42, 1982); prokaryotic expression vectors such as the beta -lactamase promoter (Villa-Kamaroff, et al., Proc. Natl. Acad. Sci. U.S.A., 75:3727-3731, 1978); or the tac promoter (DeBoer, et al., Proc. Natl. Acad. Sci. U.S.A., 80:21-25, 1983). Also of interest are the following animal transcriptional control regions, which exhibit tissue specificity and have been
35 utilized in transgenic animals: the elastase I gene control region which is active in pancreatic acinar cells (Swift et al., Cell, 38:639-646, 1984; Ornitz et al., Cold Spring Harbor Symp. Quant. Biol. 50:399-409, 1986; MacDonald, Hepatology,

7:425-515, 1987); the insulin gene control region which is active in pancreatic beta cells (Hanahan, Nature, 315:115-122, 1985); the immunoglobulin gene control region which is active in lymphoid cells (Grosschedl et al., Cell, 38:647-658, 1984; Adames et al., Nature, 318:533-538, 1985; Alexander et al., Mol. Cell. Biol., 7:1436-1444, 1987); the mouse mammary tumor virus control region which is active in testicular, breast, lymphoid and mast cells (Leder et al., Cell, 45:485-495, 1986), albumin gene control region which is active in liver (Pinkert et al., Genes and Devel., 1:268-276, 1987); the alpha-fetoprotein gene control region which is active in liver (Krumlauf et al., Mol. Cell. Biol., 5:1639-1648, 1985; Hammer et al., Science, 235:53-58, 1987); the alpha 1-antitrypsin gene control region which is active in the liver (Kelsey et al., Genes and Devel., 1:161-171, 1987); the beta-globin gene control region which is active in myeloid cells (Mogam et al., Nature, 315:338-340, 1985; Kollias et al., Cell, 46:89-94, 1986); the myelin basic protein gene control region which is active in oligodendrocyte cells in the brain (Readhead et al., Cell, 48:703-712, 1987); the myosin light chain-2 gene control region which is active in skeletal muscle (Sani, Nature, 314:283-286, 1985); and the gonadotropic releasing hormone gene control region which is active in the hypothalamus (Mason et al., Science, 234:1372-1378, 1986).

20 Enhancer Element

An enhancer sequence may be inserted into the vector to increase the transcription of a DNA sequence encoding a GDNFR protein of the present invention by higher eukaryotes. Enhancers are cis-acting elements of DNA, usually about 10-300 bp in length, that act on the promoter to increase its transcription. Enhancers are relatively orientation and position independent. They have been found 5' and 3' to the transcription unit. Several enhancer sequences available from mammalian genes are known (e.g., globin, elastase, albumin, alpha-feto-protein and insulin). Typically, however, an enhancer from a virus will be used. The SV40 enhancer, the cytomegalovirus early promoter enhancer, the polyoma enhancer, and adenovirus enhancers are exemplary enhancing elements for the activation of eukaryotic promoters. While an enhancer may be spliced into the vector at a position 5' or 3' to GDNFR DNA, it is typically located at a site 5' from the promoter.

Transcription Termination

35 Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant, animal, human, or nucleated cells from other multicellular organisms) will also contain sequences necessary for terminating transcription and stabilizing the mRNA.

Such sequences are commonly available from the 5' and occasionally 3' untranslated regions of eukaryotic DNAs or cDNAs. These regions contain nucleotide segments transcribed as polyadenylated fragments in the untranslated portion of the mRNA encoding GDNFR.

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The construction of suitable vectors containing one or more of the above-listed components together with the desired GDNFR-encoding sequence is accomplished by standard ligation techniques. Isolated plasmids or DNA fragments are cleaved, tailored, and religated in the desired order to generate the plasmids required. To confirm that the correct sequences have been constructed, the ligation mixtures may be used to transform *E. coli*, and successful transformants may be selected by known techniques, such as ampicillin or tetracycline resistance as described above. Plasmids from the transformants may then be prepared, analyzed by restriction endonuclease digestion, and/or sequenced to confirm the presence of the desired construct.

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Vectors that provide for the transient expression of DNA encoding GDNFR in mammalian cells may also be used. In general, transient expression involves the use of an expression vector that is able to replicate efficiently in a host cell, such that the host cell accumulates many copies of the expression vector and, in turn, synthesizes high levels of the desired protein encoded by the expression vector. Transient expression systems, comprising a suitable expression vector and a host cell, allow for the convenient positive identification of proteins encoded by cloned DNAs, as well as for the rapid screening of such proteins for desired biological or physiological properties. Thus, transient expression systems are particularly useful in identifying variants of the protein.

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Selection and Transformation of Host Cells

Host cells (e.g., bacterial, mammalian, insect, yeast, or plant cells) transformed with nucleic acid sequences for use in expressing a recombinant GDNFR protein are also provided by the present invention. The transformed host cell is cultured under appropriate conditions permitting the expression of the nucleic acid sequence. The selection of suitable host cells and methods for transformation, culture, amplification, screening and product production and purification are well known in the art. See for example, Gething and Sambrook, *Nature*, 293: 620-625 (1981), or alternatively, Kaufman et al., *Mol. Cell. Biol.*, 5 (7): 1750-1759 (1985) or Howley et al., U.S. Pat. No. 4,419,446. Additional exemplary materials and methods are discussed herein. The transformed host cell is cultured in a suitable medium, and

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the expressed GDNFR protein is then optionally recovered, isolated and purified from the culture medium (or from the cell, if expressed intracellularly) by an appropriate means known to those skilled in the art.

Different host cells have characteristic and specific mechanisms for the translational and post-translational processing and modification (e.g., glycosylation, cleavage) of proteins. Appropriate cell lines or host systems can be chosen to ensure the desired modification and processing of the foreign protein expressed. For example, expression in a bacterial system can be used to produce an unglycosylated core protein product. Expression in yeast may be used to produce a glycosylated product. Expression in mammalian cells can be used to ensure "native" glycosylation of the heterologous GDNFR protein. Furthermore, different vector/host expression systems may effect processing reactions such as proteolytic cleavages to different extents.

Suitable host cells for cloning or expressing the vectors disclosed herein are prokaryote, yeast, or higher eukaryote cells. Eukaryotic microbes such as filamentous fungi or yeast may be suitable hosts for the expression of GDNFR proteins. *Saccharomyces cerevisiae*, or common baker's yeast, is the most commonly used among lower eukaryotic host microorganisms, but a number of other genera, species, and strains are well known and commonly available.

Host cells to be used for the expression of glycosylated GDNFR protein are also derived from multicellular organisms. Such host cells are capable of complex processing and glycosylation activities. In principle, any higher eukaryotic cell culture might be used, whether such culture involves vertebrate or invertebrate cells, including plant and insect cells. The propagation of vertebrate cells in culture (tissue culture) is a well known procedure. Examples of useful mammalian host cell lines include, but are not limited to, monkey kidney CV1 line transformed by SV40 (COS7), human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture), baby hamster kidney cells, and Chinese hamster ovary cells. Other suitable mammalian cell lines include but are not limited to, HeLa, mouse L-929 cells, 3T3 lines derived from Swiss, Balb-c or NIH mice, BHK or HaK hamster cell lines.

Suitable host cells also include prokaryotic cells. Prokaryotic host cells include, but are not limited to, bacterial cells, such as Gram-negative or Gram-positive organisms, for example, *E. coli*, *Bacilli* such as *B. subtilis*, *Pseudomonas* species such as *P. aeruginosa*, *Salmonella typhimurium*, or *Serratia marcescans*. For example, the various strains of *E. coli* (e.g., HB101, DH5a, DH10, and MC1061) are well-known as host cells in the field of biotechnology. Various strains of

Streptomyces spp. and the like may also be employed. Presently preferred host cells for producing GDNFR proteins are bacterial cells (e.g., Escherichia coli) and mammalian cells (such as Chinese hamster ovary cells, COS cells, etc.)

5 The host cells are transfected and preferably transformed with the above-described expression or cloning vectors and cultured in a conventional nutrient medium. The medium may be modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences. Transfection and transformation are performed using standard techniques which are well known to those skilled in the art and which are selected as appropriate to the
10 host cell involved. For example, for mammalian cells without cell walls, the calcium phosphate precipitation method may be used. Electroporation, micro injection and other known techniques may also be used.

Culturing the Host Cells

15 Transformed cells used to produce GDNFR proteins of the present invention are cultured in suitable media. The media may be supplemented as necessary with hormones and/or other growth factors (such as insulin, transferrin, or epidermal growth factor), salts (such as sodium chloride, calcium, magnesium, and phosphate), buffers (such as HEPES), nucleosides (such as adenosine and thymidine), antibiotics
20 (such as gentamicin), trace elements (defined as inorganic compounds usually present at final concentrations in the micromolar range), and glucose or other energy source. Other supplements may also be included, at appropriate concentrations, as will be appreciated by those skilled in the art. Suitable culture conditions, such as temperature, pH, and the like, are also well known to those skilled in the art for use
25 with the selected host cells.

Once the GDNFR protein is produced, it may be isolated and purified by standard methods including chromatography (e.g., ion exchange, affinity, and sizing column chromatography), centrifugation, differential solubility, or by any other standard technique for the purification of proteins. For example, GDNFR- α protein
30 may be isolated by binding to an affinity column comprising GDNF or anti-GDNFR- α antibody bound to a stationary support. Similarly, GRR2 protein may be isolated by binding to an affinity column comprising neurturin or anti-GRR2 antibody bound to a stationary support.

Homologous Recombination

35 It is further envisioned that GDNFR proteins may be produced by homologous recombination, or with recombinant production methods utilizing

control elements introduced into cells already containing DNA encoding GDNFR. For example, homologous recombination methods may be used to modify a cell that contains a normally transcriptionally silent GDNFR gene or under expressed gene and thereby produce a cell which expresses GDNFR. Homologous recombination is a technique originally developed for targeting genes to induce or correct mutations in transcriptionally active genes (Kucherlapati, Prog. in Nucl. Acid Res. and Mol. Biol., 36:301, 1989). The basic technique was developed as a method for introducing specific mutations into specific regions of the mammalian genome (Thomas et al., Cell, 44:419-428, 1986; Thomas and Capecchi, Cell, 51:503-512, 1987; Doetschman et al., Proc. Natl. Acad. Sci., 85:8583-8587, 1988) or to correct specific mutations within defective genes (Doetschman et al., Nature, 330:576-578, 1987). Exemplary homologous recombination techniques are described in U.S. 5,272,071 (EP 91 90 3051, EP Publication No. 505 500; PCT/US90/07642, International Publication No. WO 91/09955) the disclosure of which is hereby incorporated by reference.

Through homologous recombination, the DNA sequence to be inserted into the genome can be directed to a specific region of the gene of interest by attaching it to targeting DNA. The targeting DNA is DNA that is complementary (homologous) to a region of the genomic DNA. Small pieces of targeting DNA that are complementary to a specific region of the genome are put in contact with the parental strand during the DNA replication process. It is a general property of DNA that has been inserted into a cell to hybridize, and therefore, recombine with other pieces of endogenous DNA through shared homologous regions. If this complementary strand is attached to an oligonucleotide that contains a mutation or a different sequence of DNA, it too is incorporated into the newly synthesized strand as a result of the recombination. As a result of the proofreading function, it is possible for the new sequence of DNA to serve as the template. Thus, the transferred DNA is incorporated into the genome.

If the sequence of a particular gene is known, such as the nucleic acid sequence, the pre-pro sequence or expression control sequence of GDNFR presented herein, a piece of DNA that is complementary to a selected region of the gene can be synthesized or otherwise obtained, such as by appropriate restriction of the native DNA at specific recognition sites bounding the region of interest. This piece serves as a targeting sequence upon insertion into the cell and will hybridize to its homologous region within the genome. If this hybridization occurs during DNA replication, this piece of DNA, and any additional sequence attached thereto, will act as an Okazaki fragment and will be backstitched into the newly synthesized daughter

strand of DNA.

Attached to these pieces of targeting DNA are regions of DNA which may interact with the expression of a GDNFR protein. For example, a promoter/enhancer element, a suppresser, or an exogenous transcription modulatory element is inserted in the genome of the intended host cell in proximity and orientation sufficient to influence the transcription of DNA encoding the desired GDNFR protein. The control element does not encode GDNFR, but instead controls a portion of the DNA present in the host cell genome. Thus, the expression of GDNFR proteins may be achieved not by transfection of DNA that encodes the GDNFR gene itself, but rather by the use of targeting DNA (containing regions of homology with the endogenous gene of interest) coupled with DNA regulatory segments that provide the endogenous gene sequence with recognizable signals for transcription of a GDNFR protein.

15 A. GDNFR variants

As discussed above, the terms "GDNFR analogs" as used herein include polypeptides in which amino acids have been deleted from ("deletion variants"), inserted into ("addition variants"), or substituted for ("substitution variants") residues within the amino acid sequence of naturally-occurring GDNFR polypeptides including those depicted in the Figures. Such variants are prepared by introducing appropriate nucleotide changes into the DNA encoding the polypeptide or by in vitro chemical synthesis of the desired polypeptide. It will be appreciated by those skilled in the art that many combinations of deletions, insertions, and substitutions can be made to an amino acid sequence such as mature human GDNFR provided that the final molecule possesses GDNFR activity.

Based upon the present description of particular GDNFR- α , GRR2 and GRR3 amino acid sequences from multiple species, as well as the consensus sequences derived therefrom, one can readily design and manufacture a variety of nucleic acid sequences suitable for use in the recombinant (e.g., microbial) expression of polypeptides having primary conformations which differ from those depicted in the Figures in terms of the identity or location of one or more residues. Mutagenesis techniques for the replacement, insertion or deletion of one or more selected amino acid residues encoded by the nucleic acid sequences depicted in Figures 2 and 4 are well known to one skilled in the art (e.g., U.S. Pat. No. 4,518,584, the disclosure of which is hereby incorporated by reference.) There are two principal variables in the construction of substitution variants: the location of the mutation site and the nature of the mutation. In designing GDNFR substitution

variants, the selection of the mutation site and nature of the mutation will depend on the GDNFR characteristic(s) to be modified. The sites for mutation can be modified individually or in series, e.g., by (1) substituting first with conservative amino acid modifications and then with more radical selections depending upon the results
5 achieved, (2) deleting the target amino acid residue, or (3) inserting amino acid residues adjacent to the located site. Conservative changes in from 1 to 30 contiguous amino acids are preferred. N-terminal and C-terminal deletion GDNFR protein variants may also be generated by proteolytic enzymes.

For GDNFR deletion variants, deletions generally range from about 1 to 30
10 contiguous residues, more usually from about 1 to 10 contiguous residues, and typically from about 1 to 5 contiguous residues. N-terminal, C-terminal and internal intrasequence deletions are contemplated. Deletions may be introduced into regions of the molecule which have low homology with non-human GDNFR to modify the activity of GDNFR. Deletions in areas of substantial homology with non-human
15 GDNFR sequences will be more likely to significantly modify GDNFR biological activity. The number of consecutive deletions typically will be selected so as to preserve the tertiary structure of the GDNFR protein product in the affected domain, e.g., cysteine crosslinking. Non-limiting examples of deletion variants include truncated GDNFR protein products lacking N-terminal or C-terminal amino acid
20 residues. For example, one may prepare a soluble receptor by elimination of the peptide region involved in a glycosyl-phosphatidylinositol (GPI) anchorage of GDNFR receptor to the cytoplasmic membrane.

For GDNFR addition variants, amino acid sequence additions typically include N-and/or C-terminal fusions or terminal additions ranging in length from one
25 residue to polypeptides containing a hundred or more residues, as well as internal or medial additions of single or multiple amino acid residues. Polypeptides of the invention may also include an initial methionine amino acid residue (at position -1 with respect to the first amino acid residue of the desired polypeptide). Internal additions may range generally from about 1 to 10 contiguous residues, more
30 typically from about 1 to 5 residues, and usually from about 1 to 3 amino acid residues. Examples of N-terminal addition variants include GDNFR with the inclusion of a heterologous N-terminal signal sequence to the N-terminus of GDNFR to facilitate the secretion of mature GDNFR from recombinant host cells and thereby facilitate harvesting or bioavailability. Such signal sequences generally will be
35 obtained from, and thus be homologous to, the intended host cell species. Additions may also include amino acid sequences derived from the sequence of other neurotrophic factors. For example, it is contemplated that a fusion protein of GDNF

and GDNFR- α , or neurturin and GRR2, may be produced, with or without a linking sequence, thereby forming a single molecule therapeutic entity.

GDNFR substitution variants have one or more amino acid residues of the GDNFR amino acid sequence removed and a different residue(s) inserted in its place. Such substitution variants include allelic variants, which are characterized by naturally-occurring nucleotide sequence changes in the species population that may or may not result in an amino acid change. As with the other variant forms, substitution variants may involve the replacement of single or contiguous amino acid residues at one or more different locations.

Specific mutations of the GDNFR amino acid sequence may involve modifications to a glycosylation site (e.g., serine, threonine, or asparagine). The absence of glycosylation or only partial glycosylation results from amino acid substitution or deletion at any asparagine-linked glycosylation recognition site or at any site of the molecule that is modified by addition of an O-linked carbohydrate. An asparagine-linked glycosylation recognition site comprises a tripeptide sequence which is specifically recognized by appropriate cellular glycosylation enzymes. These tripeptide sequences are either Asn-Xaa-Thr or Asn-Xaa-Ser, where Xaa can be any amino acid other than Pro. A variety of amino acid substitutions or deletions at one or both of the first or third amino acid positions of a glycosylation recognition site (and/or amino acid deletion at the second position) result in non-glycosylation at the modified tripeptide sequence. Thus, the expression of appropriate altered nucleotide sequences produces variants which are not glycosylated at that site. Alternatively, the GDNFR amino acid sequence may be modified to add glycosylation sites.

One method for identifying GDNFR amino acid residues or regions for mutagenesis is called "alanine scanning mutagenesis" as described by Cunningham and Wells (Science, 244: 1081-1085, 1989). In this method, an amino acid residue or group of target residues are identified (e.g., charged residues such as Arg, Asp, His, Lys, and Glu) and replaced by a neutral or negatively charged amino acid (most preferably alanine or polyalanine) to affect the interaction of the amino acids with the surrounding aqueous environment in or outside the cell. Those domains demonstrating functional sensitivity to the substitutions may then be refined by introducing additional or alternate residues at the sites of substitution. Thus, the target site for introducing an amino acid sequence variation is determined, alanine scanning or random mutagenesis is conducted on the corresponding target codon or region of the DNA sequence, and the expressed GDNFR variants are screened for the optimal combination of desired activity and degree of activity.

The sites of greatest interest for substitutional mutagenesis include sites where the amino acids found in GDNFR proteins from various species are substantially different in terms of side-chain bulk, charge, and/or hydrophobicity. Other sites of interest are those in which particular residues of GDNFR-like proteins, obtained from various species, are identical. Such positions are generally important for the biological activity of a protein. Initially, these sites are substituted in a relatively conservative manner. Such conservative substitutions are shown in Table 2 under the heading of preferred substitutions. If such substitutions result in a change in biological activity, then more substantial changes (exemplary substitutions) may be introduced, and/or other additions or deletions may be made, and the resulting products are screened for activity.

TABLE 2
Amino Acid Substitutions

15

<u>Original Residue</u>	<u>Preferred Substitutions</u>	<u>Exemplary Substitutions</u>
Ala (A)	Val	Val; Leu; Ile
Arg (R)	Lys	Lys; Gln; Asn
Asn (N)	Gln	Gln; His; Lys; Arg
Asp (D)	Glu	Glu
Cys (C)	Ser	Ser
Gln (Q)	Asn	Asn
Glu (E)	Asp	Asp
Gly (G)	Pro	Pro
His (H)	Arg	Asn; Gln; Lys; Arg
Ile (I)	Leu	Leu; Val; Met; Ala; Phe; norleucine
Leu (L)	Ile	norleucine; Ile; Val; Met; Ala; Phe
Lys (K)	Arg	Arg; Gln; Asn
Met (M)	Leu	Leu; Phe; Ile
Phe (F)	Leu	Leu; Val; Ile; Ala
Pro (P)	Gly	Gly
Ser (S)	Thr	Thr
Thr (T)	Ser	Ser
Trp (W)	Tyr	Tyr

Tyr (Y)	Phe	Trp; Phe; Thr; Ser
Val (V)	Leu	Ile; Leu; Met; Phe; Ala; norleucine

Conservative modifications to the amino acid sequence (and the corresponding modifications to the encoding nucleic acid sequences) are expected to produce GDNFR protein products having functional and chemical characteristics similar to those of naturally occurring GDNFR. In contrast, substantial modifications in the functional and/or chemical characteristics of GDNFR protein products may be accomplished by selecting substitutions that differ significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. Naturally occurring residues may be divided into groups based on common side chain properties:

- 1) hydrophobic: norleucine, Met, Ala, Val, Leu, Ile;
- 2) neutral hydrophilic: Cys, Ser, Thr;
- 3) acidic: Asp, Glu;
- 4) basic: Asn, Gln, His, Lys, Arg;
- 5) residues that influence chain orientation: Gly, Pro; and
- 6) aromatic: Trp, Tyr, Phe.

Non-conservative substitutions may involve the exchange of a member of one of these classes for a member from another class. Such substituted residues may be introduced into regions of the human GDNFR protein that are homologous with non-human GDNFR proteins, or into the non-homologous regions of the molecule.

Thus, GDNFR proteins include those biologically active molecules containing all or part of the amino acid sequences as depicted in the Figures, as well as consensus and modified sequences in which biologically equivalent amino acid residues are substituted for residues within the sequence resulting in a silent change. For example, one or more amino acid residues within the sequence can be substituted by another amino acid of a similar polarity which acts as a functional equivalent, resulting in a silent alteration. Substitutes for an amino acid within the sequence may be selected from other members of the class to which the amino acid belongs. For example, the nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan and methionine. The polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine. The positively charged (basic) amino acids include arginine, lysine

and histidine. The negatively charged (acidic) amino acids include aspartic acid and glutamic acid. It is also contemplated that the GDNFR proteins, analogs, or fragments or derivatives thereof may be differentially modified during or after translation, e.g., by phosphorylation, glycosylation, crosslinking, acylation, proteolytic cleavage, linkage to an antibody molecule, membrane molecule or other ligand.

B. GDNFR Derivatives

Chemically modified derivatives of GDNFR or GDNFR analogs may be prepared by one of skill in the art based upon the present disclosure. The chemical moieties most suitable for derivatization include water soluble polymers. A water soluble polymer is desirable because the protein to which it is attached does not precipitate in an aqueous environment, such as a physiological environment. Preferably, the polymer will be pharmaceutically acceptable for the preparation of a therapeutic product or composition. One skilled in the art will be able to select the desired polymer based on such considerations as whether the polymer/protein conjugate will be used therapeutically, and if so, the desired dosage, circulation time, resistance to proteolysis, and other considerations. The effectiveness of the derivatization may be ascertained by administering the derivative, in the desired form (e.g., by osmotic pump, or, more preferably, by injection or infusion, or, further formulated for oral, pulmonary or other delivery routes), and determining its effectiveness.

Suitable water soluble polymers include, but are not limited to, polyethylene glycol, copolymers of ethylene glycol/propylene glycol, carboxymethylcellulose, dextran, polyvinyl alcohol, polyvinyl pyrrolidone, poly-1, 3-dioxolane, poly-1,3,6-trioxane, ethylene/maleic anhydride copolymer, polyaminoacids (either homopolymers or random copolymers), and dextran or poly(n-vinyl pyrrolidone)polyethylene glycol, propylene glycol homopolymers, propylene oxide/ethylene oxide co-polymers, polyoxyethylated polyols (e.g., glycerol), polyvinyl alcohol, and mixtures thereof. Polyethylene glycol propionaldehyde may have advantages in manufacturing due to its stability in water.

The polymer may be of any molecular weight, and may be branched or unbranched. For polyethylene glycol, the preferred molecular weight is between about 2 kDa and about 100 kDa for ease in handling and manufacturing (the term "about" indicating that in preparations of polyethylene glycol, some molecules will weigh more, some less, than the stated molecular weight). Other sizes may be used, depending on the desired therapeutic profile (e.g., the duration of sustained release

desired; the effects, if any, on biological activity; the ease in handling; the degree or lack of antigenicity and other known effects of polyethylene glycol on a therapeutic protein or variant).

5 The number of polymer molecules so attached may vary, and one skilled in the art will be able to ascertain the effect on function. One may mono-derivatize, or may provide for a di-, tri-, tetra- or some combination of derivatization, with the same or different chemical moieties (e.g., polymers, such as different weights of polyethylene glycols). The proportion of polymer molecules to protein (or peptide) molecules will vary, as will their concentrations in the reaction mixture. In general,
10 the optimum ratio (in terms of efficiency of reaction in that there is no excess unreacted protein or polymer) will be determined by factors such as the desired degree of derivatization (e.g., mono, di-, tri-, etc.), the molecular weight of the polymer selected, whether the polymer is branched or unbranched, and the reaction conditions.

15 The polyethylene glycol molecules (or other chemical moieties) should be attached to the protein with consideration of effects on functional or antigenic domains of the protein. There are a number of attachment methods available to those skilled in the art. See for example, EP 0 401 384, the disclosure of which is hereby incorporated by reference (coupling PEG to G-CSF), see also Malik et al., Exp.
20 Hematol., 20: 1028-1035, 1992 (reporting pegylation of GM-CSF using tresyl chloride). For example, polyethylene glycol may be covalently bound through amino acid residues via a reactive group, such as, a free amino or carboxyl group. Reactive groups are those to which an activated polyethylene glycol molecule may be bound. The amino acid residues having a free amino group may include lysine
25 residues and the N-terminal amino acid residue. Those having a free carboxyl group may include aspartic acid residues, glutamic acid residues, and the C-terminal amino acid residue. Sulfhydryl groups may also be used as a reactive group for attaching the polyethylene glycol molecule(s). For therapeutic purposes, attachment at an amino group, such as attachment at the N-terminus or lysine group is preferred. Attachment
30 at residues important for receptor binding should be avoided if receptor binding is desired.

One may specifically desire an N-terminal chemically modified protein. Using polyethylene glycol as an illustration of the present compositions, one may select from a variety of polyethylene glycol molecules (by molecular weight,
35 branching, etc.), the proportion of polyethylene glycol molecules to protein (or peptide) molecules in the reaction mix, the type of pegylation reaction to be performed, and the method of obtaining the selected N-terminally pegylated protein.

The method of obtaining the N-terminally pegylated preparation (i.e., separating this moiety from other monopegylated moieties if necessary) may be by purification of the N-terminally pegylated material from a population of pegylated protein molecules. Selective N-terminal chemical modification may be accomplished by
5 reductive alkylation which exploits differential reactivity of different types of primary amino groups (lysine versus the N-terminal) available for derivatization in a particular protein. Under the appropriate reaction conditions, substantially selective derivatization of the protein at the N-terminus with a carbonyl group containing polymer is achieved. For example, one may selectively N-terminally pegylate the
10 protein by performing the reaction at a pH which allows one to take advantage of the pKa differences between the ϵ -amino group of the lysine residues and that of the α -amino group of the N-terminal residue of the protein. By such selective derivatization, attachment of a water soluble polymer to a protein is controlled: the conjugation with the polymer takes place predominantly at the N-terminus of the
15 protein and no significant modification of other reactive groups, such as the lysine side chain amino groups, occurs. Using reductive alkylation, the water soluble polymer may be of the type described above, and should have a single reactive aldehyde for coupling to the protein. Polyethylene glycol propionaldehyde, containing a single reactive aldehyde, may be used.

20 The present invention contemplates use of derivatives which are prokaryote-expressed GDNFR proteins, or variants thereof, linked to at least one polyethylene glycol molecule, as well as use of GDNFR proteins, or variants thereof, attached to one or more polyethylene glycol molecules via an acyl or alkyl linkage.

Pegylation may be carried out by any of the pegylation reactions known in
25 the art. See, for example: Focus on Growth Factors, 3 (2): 4-10, 1992; EP 0 154 316, the disclosure of which is hereby incorporated by reference; EP 0 401 384; and the other publications cited herein that relate to pegylation. The pegylation may be carried out via an acylation reaction or an alkylation reaction with a reactive polyethylene glycol molecule (or an analogous reactive water-soluble polymer).

30 Pegylation by acylation generally involves reacting an active ester derivative of polyethylene glycol (PEG) with the GDNFR protein or variant. Any known or subsequently discovered reactive PEG molecule may be used to carry out the pegylation of GDNFR protein or variant. A preferred activated PEG ester is PEG esterified to N-hydroxysuccinimide (NHS). As used herein, "acylation" is
35 contemplated to include without limitation the following types of linkages between the therapeutic protein and a water soluble polymer such as PEG: amide, carbamate, urethane, and the like. See Bioconjugate Chem., 5: 133-140, 1994. Reaction

conditions may be selected from any of those known in the pegylation art or those subsequently developed, but should avoid conditions such as temperature, solvent, and pH that would inactivate the GDNFR or variant to be modified.

Pegylation by acylation will generally result in a poly-pegylated GDNFR protein or variant. Preferably, the connecting linkage will be an amide. Also preferably, the resulting product will be substantially only (e.g., > 95%) mono, di- or tri-pegylated. However, some species with higher degrees of pegylation may be formed in amounts depending on the specific reaction conditions used. If desired, more purified pegylated species may be separated from the mixture, particularly unreacted species, by standard purification techniques, including, among others, dialysis, salting-out, ultrafiltration, ion-exchange chromatography, gel filtration chromatography and electrophoresis.

Pegylation by alkylation generally involves reacting a terminal aldehyde derivative of PEG with the GDNFR protein or variant in the presence of a reducing agent. Pegylation by alkylation can also result in poly-pegylated GDNFR protein or variant. In addition, one can manipulate the reaction conditions to favor pegylation substantially only at the α -amino group of the N-terminus of the GDNFR protein or variant (i.e., a mono-pegylated protein). In either case of monopegylation or polypegylation, the PEG groups are preferably attached to the protein via a $-\text{CH}_2\text{-NH}-$ group. With particular reference to the $-\text{CH}_2-$ group, this type of linkage is referred to herein as an "alkyl" linkage.

Derivatization via reductive alkylation to produce a monopegylated product exploits differential reactivity of different types of primary amino groups (lysine versus the N-terminal) available for derivatization. The reaction is performed at a pH which allows one to take advantage of the pKa differences between the ϵ -amino groups of the lysine residues and that of the α -amino group of the N-terminal residue of the protein. By such selective derivatization, attachment of a water soluble polymer that contains a reactive group such as an aldehyde, to a protein is controlled: the conjugation with the polymer takes place predominantly at the N-terminus of the protein and no significant modification of other reactive groups, such as the lysine side chain amino groups, occurs. In one important aspect, the present invention contemplates use of a substantially homogeneous preparation of monopolymer/GDNFR protein (or variant) conjugate molecules (meaning GDNFR protein or variant to which a polymer molecule has been attached substantially only (i.e., > 95%) in a single location). More specifically, if polyethylene glycol is used, the present invention also encompasses use of pegylated GDNFR protein or variant lacking possibly antigenic linking groups, and having the polyethylene glycol

molecule directly coupled to the GDNFR protein or variant.

Thus, GDNFR protein products according to the present invention include pegylated GDNFR protein or variants, wherein the PEG group(s) is (are) attached via acyl or alkyl groups. As discussed above, such products may be mono-pegylated or poly-pegylated (e.g., containing 2-6, and preferably 2-5, PEG groups). The PEG groups are generally attached to the protein at the α - or ϵ -amino groups of amino acids, but it is also contemplated that the PEG groups could be attached to any amino group attached to the protein, which is sufficiently reactive to become attached to a PEG group under suitable reaction conditions.

The polymer molecules used in both the acylation and alkylation approaches may be selected from among water soluble polymers as described above. The polymer selected should be modified to have a single reactive group, such as an active ester for acylation or an aldehyde for alkylation, preferably, so that the degree of polymerization may be controlled as provided for in the present methods. An exemplary reactive PEG aldehyde is polyethylene glycol propionaldehyde, which is water stable, or mono C1-C10 alkoxy or aryloxy derivatives thereof (see, U.S. Patent 5,252,714). The polymer may be branched or unbranched. For the acylation reactions, the polymer(s) selected should have a single reactive ester group. For the present reductive alkylation, the polymer(s) selected should have a single reactive aldehyde group. Generally, the water soluble polymer will not be selected from naturally-occurring glycosyl residues since these are usually made more conveniently by mammalian recombinant expression systems. The polymer may be of any molecular weight, and may be branched or unbranched.

An exemplary water-soluble polymer for use herein is polyethylene glycol. As used herein, polyethylene glycol is meant to encompass any of the forms of PEG that have been used to derivatize other proteins, such as mono-(C1-C10) alkoxy- or aryloxy-polyethylene glycol.

In general, chemical derivatization may be performed under any suitable condition used to react a biologically active substance with an activated polymer molecule. Methods for preparing a pegylated GDNFR protein product will generally comprise the steps of (a) reacting a GDNFR protein product with polyethylene glycol (such as a reactive ester or aldehyde derivative of PEG) under conditions whereby the protein becomes attached to one or more PEG groups, and (b) obtaining the reaction product(s). In general, the optimal reaction conditions for the acylation reactions will be determined case-by-case based on known parameters and the desired result. For example, the larger the ratio of PEG:protein, the greater the percentage of poly-pegylated product.

Reductive alkylation to produce a substantially homogeneous population of mono-polymer/GDNFR protein product will generally comprise the steps of:

- (a) reacting a GDNFR protein or variant with a reactive PEG molecule under reductive alkylation conditions, at a pH suitable to permit selective modification of the α -amino group at the amino terminus of said GDNFR protein or variant; and
- (b) obtaining the reaction product(s).

For a substantially homogeneous population of mono-polymer/GDNFR protein product, the reductive alkylation reaction conditions are those which permit the selective attachment of the water soluble polymer moiety to the N-terminus of GDNFR protein or variant. Such reaction conditions generally provide for pKa differences between the lysine amino groups and the α -amino group at the N-terminus (the pKa being the pH at which 50% of the amino groups are protonated and 50% are not). The pH also affects the ratio of polymer to protein to be used. In general, if the pH is lower, a larger excess of polymer to protein will be desired (i.e., the less reactive the N-terminal α -amino group, the more polymer needed to achieve optimal conditions). If the pH is higher, the polymer:protein ratio need not be as large (i.e., more reactive groups are available, so fewer polymer molecules are needed). For purposes of the present invention, the pH will generally fall within the range of 3-9, preferably 3-6.

Another important consideration is the molecular weight of the polymer. In general, the higher the molecular weight of the polymer, the fewer polymer molecules may be attached to the protein. Similarly, branching of the polymer should be taken into account when optimizing these parameters. Generally, the higher the molecular weight (or the more branches) the higher the polymer:protein ratio. In general, for the pegylation reactions contemplated herein, the preferred average molecular weight is about 2 kDa to about 100 kDa. The preferred average molecular weight is about 5 kDa to about 50 kDa, particularly preferably about 12 kDa to about 25 kDa. The ratio of water-soluble polymer to GDNF protein or variant will generally range from 1:1 to 100:1, preferably (for polypegylation) 1:1 to 20:1 and (for monopegylation) 1:1 to 5:1.

Using the conditions indicated above, reductive alkylation will provide for selective attachment of the polymer to any GDNFR protein or variant having an α -amino group at the amino terminus, and provide for a substantially homogenous preparation of monopolymer/GDNFR protein (or variant) conjugate. The term "monopolymer/GDNFR protein (or variant) conjugate" is used here to mean a composition comprised of a single polymer molecule attached to a molecule of GDNFR protein or GDNFR variant protein. The monopolymer/GDNFR protein (or

variant) conjugate typically will have a polymer molecule located at the N-terminus, but not on lysine amino side groups. The preparation will generally be greater than 90% monopolymer/GDNFR protein (or variant) conjugate, and more usually greater than 95% monopolymer/GDNFR protein (or variant) conjugate, with the remainder
5 of observable molecules being unreacted (i.e., protein lacking the polymer moiety). It is also envisioned that the GDNFR protein product may involve the preparation of a pegylated molecule involving a fusion protein or linked GDNFR and neurotrophic factor, such as GDNFR- α and GDNF molecules or GRR2 and neurturin molecules.

For the present reductive alkylation, the reducing agent should be stable in
10 aqueous solution and preferably be able to reduce only the Schiff base formed in the initial process of reductive alkylation. Suitable reducing agents may be selected from sodium borohydride, sodium cyanoborohydride, dimethylamine borane, trimethylamine borane and pyridine borane. A particularly suitable reducing agent is sodium cyanoborohydride. Other reaction parameters, such as solvent, reaction
15 times, temperatures, etc., and means of purification of products, can be determined case-by-case based on the published information relating to derivatization of proteins with water soluble polymers (see the publications cited herein).

C. GDNFR Protein Product Pharmaceutical Compositions

20 GDNFR protein product pharmaceutical compositions typically include a therapeutically or prophylactically effective amount of GDNFR protein product in admixture with one or more pharmaceutically and physiologically acceptable formulation materials selected for suitability with the mode of administration. Suitable formulation materials include, but are not limited to, antioxidants,
25 preservatives, coloring, flavoring and diluting agents, emulsifying agents, suspending agents, solvents, fillers, bulking agents, buffers, delivery vehicles, diluents, excipients and/or pharmaceutical adjuvants. For example, a suitable vehicle may be water for injection, physiological saline solution, or artificial cerebrospinal fluid, possibly supplemented with other materials common in
30 compositions for parenteral administration. Neutral buffered saline or saline mixed with serum albumin are further exemplary vehicles. The term "pharmaceutically acceptable carrier" or "physiologically acceptable carrier" as used herein refers to a formulation material(s) suitable for accomplishing or enhancing the delivery of the GDNFR protein product as a pharmaceutical composition.

35 The primary solvent in a vehicle may be either aqueous or non-aqueous in nature. In addition, the vehicle may contain other formulation materials for modifying or maintaining the pH, osmolarity, viscosity, clarity, color, sterility,

stability, rate of dissolution, or odor of the formulation. Similarly, the vehicle may contain additional formulation materials for modifying or maintaining the rate of release of GDNFR protein product, or for promoting the absorption or penetration of GDNFR protein product across the blood-brain barrier.

5 Once the therapeutic pharmaceutical composition has been formulated, it may be stored in sterile vials as a solution, suspension, gel, emulsion, solid, or dehydrated or lyophilized powder. Such formulations may be stored either in a ready to use form or in a form (e.g., lyophilized) requiring reconstitution prior to administration.

10 The optimal pharmaceutical formulation will be determined by one skilled in the art depending upon the intended route of administration and desired dosage. See for example, Remington's Pharmaceutical Sciences, 18th Ed. (1990, Mack Publishing Co., Easton, PA 18042) pages 1435-1712, the disclosure of which is hereby incorporated by reference. Such compositions may influence the physical
15 state, stability, rate of in vivo release, and rate of in vivo clearance of the present proteins and derivatives.

Effective administration forms, such as (1) slow-release formulations, (2) inhalant mists, or (3) orally active formulations are envisioned. The GDNFR protein product pharmaceutical composition also may be formulated for parenteral
20 administration. Such parenterally administered therapeutic compositions are typically in the form of a pyrogen-free, parenterally acceptable aqueous solution comprising the GDNFR protein product in a pharmaceutically acceptable vehicle. One preferred vehicle is physiological saline. The GDNFR protein product pharmaceutical compositions also may include particulate preparations of polymeric
25 compounds such as polylactic acid, polyglycolic acid, etc. or into liposomes. Hyaluronic acid may also be used, and this may have the effect of promoting sustained duration in the circulation.

A particularly suitable vehicle for parenteral injection is sterile distilled water in which the GDNFR protein product is formulated as a sterile, isotonic solution,
30 properly preserved. Yet another preparation may involve the formulation of the GDNFR protein product with an agent, such as injectable microspheres or liposomes, that provides for the slow or sustained release of the protein which may then be delivered as a depot injection. Other suitable means for the introduction of GDNFR protein product include implantable drug delivery devices which contain the
35 GDNFR protein product.

The preparations of the present invention may include other components, for example parenterally acceptable preservatives, tonicity agents, cosolvents, wetting

agents, complexing agents, buffering agents, antimicrobials, antioxidants and surfactants, as are well known in the art. For example, suitable tonicity enhancing agents include alkali metal halides (preferably sodium or potassium chloride), mannitol, sorbitol and the like. Suitable preservatives include, but are not limited to, benzalkonium chloride, thimerosal, phenethyl alcohol, methylparaben, propylparaben, chlorhexidine, sorbic acid and the like. Hydrogen peroxide may also be used as preservative. Suitable cosolvents are for example glycerin, propylene glycol and polyethylene glycol. Suitable complexing agents are for example caffeine, polyvinylpyrrolidone, beta-cyclodextrin or hydroxypropyl-beta-cyclodextrin. Suitable surfactants or wetting agents include sorbitan esters, polysorbates such as polysorbate 80, tromethamine, lecithin, cholesterol, tyloxapal and the like. The buffers can be conventional buffers such as borate, citrate, phosphate, bicarbonate, or Tris-HCl.

The formulation components are present in concentration that are acceptable to the site of administration. For example, buffers are used to maintain the composition at physiological pH or at slightly lower pH, typically within a pH range of from about 5 to about 8.

A pharmaceutical composition may be formulated for inhalation. For example, the GDNFR protein product may be formulated as a dry powder for inhalation. GDNFR protein product inhalation solutions may also be formulated in a liquefied propellant for aerosol delivery. In yet another formulation, solutions may be nebulized.

It is also contemplated that certain formulations containing GDNFR protein product are to be administered orally. GDNFR protein product which is administered in this fashion may be formulated with or without those carriers customarily used in the compounding of solid dosage forms such as tablets and capsules. For example, a capsule may be designed to release the active portion of the formulation at the point in the gastrointestinal tract when bioavailability is maximized and pre-systemic degradation is minimized. Additional formulation materials may be included to facilitate absorption of GDNFR protein product. Diluents, flavorings, low melting point waxes, vegetable oils, lubricants, suspending agents, tablet disintegrating agents, and binders may also be employed.

Another preparation may involve an effective quantity of GDNFR protein product in a mixture with non-toxic excipients which are suitable for the manufacture of tablets. By dissolving the tablets in sterile water, or other appropriate vehicle, solutions can be prepared in unit dose form. Suitable excipients include, but are not limited to, inert diluents, such as calcium carbonate, sodium

carbonate or bicarbonate, lactose, or calcium phosphate; or binding agents, such as starch, gelatin, or acacia; or lubricating agents such as magnesium stearate, stearic acid, or talc.

Additional GDNFR protein product formulations will be evident to those skilled in the art, including formulations involving GDNFR protein product in combination with GDNF protein product. Techniques for formulating a variety of other sustained- or controlled-delivery means, such as liposome carriers, bio-erodible microparticles or porous beads and depot injections, are also known to those skilled in the art. See, for example, Supersaxo et al. description of controlled release porous polymeric microparticles for the delivery of pharmaceutical compositions (International Publication No. WO 93/15722; International Application No. PCT/US93/00829) the disclosure of which is hereby incorporated by reference.

D. Administration of GDNFR Protein Product

The GDNFR protein product may be administered parenterally via a variety of routes, including subcutaneous, intramuscular, intravenous, transpulmonary, transdermal, intrathecal and intracerebral delivery. In addition, protein factors that do not readily cross the blood-brain barrier may be given directly intracerebrally or otherwise in association with other elements that will transport them across the barrier. For example, the GDNFR protein product may be administered intracerebroventricularly or into the brain or spinal cord subarachnoid space. GDNFR protein product may also be administered intracerebrally directly into the brain parenchyma. GDNFR protein product may be administered extracerebrally in a form that has been modified chemically or packaged so that it passes the blood-brain barrier, or with one or more agents capable of promoting penetration of GDNFR protein product across the barrier. For example, a conjugate of NGF and monoclonal anti-transferrin receptor antibodies has been shown to be transported to the brain via binding to transferrin receptors.

To achieve the desired level of GDNFR protein product, repeated daily or less frequent injections may be administered, or GDNFR protein product may be infused continuously or periodically from a constant- or programmable-flow implanted pump. Slow-releasing implants containing the neurotrophic factor embedded in a biodegradable polymer matrix can also deliver GDNFR protein product. The frequency of dosing will depend on the pharmacokinetic parameters of the GDNFR protein product as formulated, and the route and site of administration.

Regardless of the manner of administration, the specific dose may be calculated according to body weight, body surface area or organ size. Further

refinement of the calculations necessary to determine the appropriate dosage for treatment involving each of the above mentioned formulations is routinely made by those of ordinary skill in the art and is within the ambit of tasks routinely performed by them. Appropriate dosages may be ascertained through use of appropriate dose-response data.

The final dosage regimen involved in a method for treating a specific injury or condition will be determined by the attending physician. Generally, an effective amount of the GDNFR protein product will be determined by considering various factors which modify the action of drugs, e.g., the age, condition, body weight, sex and diet of the patient, the severity of any infection, time of administration and other clinical factors. See, Remington's Pharmaceutical Sciences, supra, at pages 697-773, herein incorporated by reference. For example, it is contemplated that if GDNFR- α is used to enhance GDNF action, then the GDNFR- α dose is selected to be similar to that required for GDNF therapy; if GDNFR- α is used to antagonize GDNF action, then the GDNFR- α dose would be several times the GDNF dose. Dosing may be one or more times daily, or less frequently, and may be in conjunction with other compositions as described herein. It should be noted that the present invention is not limited to the dosages recited herein.

It is envisioned that the continuous administration or sustained delivery of GDNFR protein products may be advantageous for a given treatment. While continuous administration may be accomplished via a mechanical means, such as with an infusion pump, it is contemplated that other modes of continuous or near continuous administration may be practiced. For example, chemical derivatization or encapsulation may result in sustained release forms of the protein which have the effect of continuous presence in the bloodstream, in predictable amounts, based on a determined dosage regimen. Thus, GDNFR protein products include proteins derivatized or otherwise formulated to effectuate such continuous administration. Sustained release forms of the GDNFR protein products will be formulated to provide the desired daily or weekly effective dosage.

It is further contemplated that the GDNFR protein product may be administered in a combined form with GDNF and/or neurturin. Alternatively, the GDNFR protein product may be administered separately from a neurotrophic factor, either sequentially or simultaneously.

GDNFR protein product of the present invention may also be employed, alone or in combination with other growth factors in the treatment of nerve disease. In addition, other factors or other molecules, including chemical compositions, may be employed together with a GDNFR protein product. For example, in the treatment

of Parkinson's Disease, it is contemplated that GDNFR protein product be used by itself or in conjunction with the administration of Levodopa, wherein the GDNFR would enhance the activity of endogenous GDNF and thereby enhance the neuronal uptake of the increased concentration of dopamine.

5 As stated above, it is also contemplated that additional neurotrophic or neuron nurturing factors will be useful or necessary to treat some neuronal cell populations or some types of injury or disease. Other factors that may be used in conjunction with GDNFR or a combination of GDNFR and a neurotrophic factor such as GDNF or neurturin include, but are not limited to: mitogens such as insulin,
10 insulin-like growth factors, epidermal growth factor, vasoactive growth factor, pituitary adenylate cyclase activating polypeptide, interferon and somatostatin; neurotrophic factors such as nerve growth factor, brain derived neurotrophic factor, neurotrophin-3, neurotrophin-4/5, neurotrophin-6, insulin-like growth factor, ciliary neurotrophic factor, acidic and basic fibroblast growth factors, fibroblast growth
15 factor-5, transforming growth factor- β , cocaine-amphetamine regulated transcript (CART); and other growth factors such as epidermal growth factor, leukemia inhibitory factor, interleukins, interferons, and colony stimulating factors; as well as molecules and materials which are the functional equivalents to these factors.

20 GDNFR Protein Product Cell Therapy and Gene Therapy

GDNFR protein product cell therapy, e.g., intracerebral implantation of cells producing GDNFR protein product, is also contemplated. This embodiment would involve implanting into patients cells capable of synthesizing and secreting a biologically active form of GDNFR protein product. Such GDNFR protein product-
25 producing cells may be cells that are natural producers of GDNFR protein product or may be recombinant cells whose ability to produce GDNFR protein product has been augmented by transformation with a gene encoding the desired GDNFR protein product. Such a modification may be accomplished by means of a vector suitable for delivering the gene as well as promoting its expression and secretion. In order to
30 minimize a potential immunological reaction in patients being administered a GDNFR protein product of a foreign species, it is preferred that the natural cells producing GDNFR protein product be of human origin and produce human GDNFR protein product. Likewise, it is preferred that the recombinant cells producing GDNFR protein product be transformed with an expression vector containing a gene
35 encoding a human GDNFR protein product.

Implanted cells may be encapsulated to avoid infiltration of surrounding tissue. Human or non-human animal cells may be implanted in patients in

biocompatible, semipermeable polymeric enclosures or membranes that allow release of GDNFR protein product, but that prevent destruction of the cells by the patient's immune system or by other detrimental factors from the surrounding tissue. Alternatively, the patient's own cells, transformed to produce GDNFR protein product ex vivo, could be implanted directly into the patient without such encapsulation.

Techniques for the encapsulation of living cells are familiar to those of ordinary skill in the art, and the preparation of the encapsulated cells and their implantation in patients may be accomplished without undue experimentation. For example, Baetge et al. (International Publication No. WO 95/05452; International Application No. PCT/US94/09299 the disclosure of which is hereby incorporated by reference) describe biocompatible capsules containing genetically engineered cells for the effective delivery of biologically active molecules. In addition, see U.S. Patent Numbers 4,892,538, 5,011,472, and 5,106,627, each of which is specifically incorporated herein by reference. A system for encapsulating living cells is described in PCT Application WO 91/10425 of Aebischer et al., specifically incorporated herein by reference. See also, PCT Application WO 91/10470 of Aebischer et al., Winn et al., *Exper. Neurol.*, 113:322-329, 1991, Aebischer et al., *Exper. Neurol.*, 111:269-275, 1991; Tresco et al., *ASAIO*, 38:17-23, 1992, each of which is specifically incorporated herein by reference.

In vivo and in vitro gene therapy delivery of GDNFR protein product is also envisioned. In vitro gene therapy may be accomplished by introducing the gene coding for GDNFR protein product into targeted cells via local injection of a nucleic acid construct or other appropriate delivery vectors. (Hefti, *J. Neurobiol.*, 25:1418-1435, 1994). For example, a nucleic acid sequence encoding a GDNFR protein product may be contained in an adeno-associated virus vector for delivery into the targeted cells (e.g., Johnson, International Publication No. WO 95/34670; International Application No. PCT/US95/07178 the disclosure of which is hereby incorporated by reference). Alternative viral vectors include, but are not limited to, retrovirus, adenovirus, herpes simplex virus and papilloma virus vectors. Physical transfer, either in vivo or ex vivo as appropriate, may also be achieved by liposome-mediated transfer, direct injection (naked DNA), receptor-mediated transfer (ligand-DNA complex), electroporation, calcium phosphate precipitation or microparticle bombardment (gene gun).

It is also contemplated that GDNFR protein product gene therapy or cell therapy can further include the delivery of GDNF protein product. For example, the host cell may be modified to express and release both GDNFR- α protein product and

GDNF, or GRR2 and neurturin. Alternatively, the GDNFR- α and GDNF protein products, or GRR2 and neurturin, may be expressed in and released from separate cells. Such cells may be separately introduced into the patient or the cells may be contained in a single implantable device, such as the encapsulating membrane
5 described above.

It should be noted that the GDNFR protein product formulations described herein may be used for veterinary as well as human applications and that the term "patient" should not be construed in a limiting manner. In the case of veterinary
10 applications, the dosage ranges may be determined as described above.

EXAMPLES

15

Example 1

Identification of Cells Expressing High Affinity GDNF Binding Sites

Expression cloning involved the selection of a source of mRNA which is likely to contain significant levels of the target transcript. Retina photoreceptor cells
20 were identified as responsive to GDNF at very low concentrations, suggesting the existence of a functional, high affinity receptor. To confirm that rat photoreceptor cells did express a high affinity receptor for GDNF, [125 I]GDNF binding and photographic emulsion analysis were carried out.

25 Rat Retinal Cell Cultures

The neural retinas of 5-day-old C57Bl/6 mouse pups or 3-day-old Sprague-Dawley rat pups (Jackson Laboratories, Bar Harbor, MA) were carefully removed and dissected free of the pigment epithelium, cut into 1 mm² fragments and placed into ice-cold phosphate-buffered saline (PBS). The retinas were then transferred into
30 10 mL of Hank's balanced salt solution (HBSS) containing 120 units papain and 2000 units DNAase and incubated for 20 minutes at 37°C on a rotary platform shaker at about 200 rpm. The cells were then dispersed by trituration through fire-polished Pasteur pipettes, sieved through a 20 μ m Nitex nylon mesh and centrifuged for five minutes at 200 x g. The resulting cell pellet was resuspended into HBSS
35 containing 1% ovalbumin and 500 units DNAase, layered on top of a 4 % ovalbumin solution (in HBSS) and centrifuged for 10 minutes at 500 x g. The final pellet was resuspended in complete culture medium (see below), adjusted to about 15,000

cells/mL, and seeded in 90 µl aliquots into tissue culture plates coated with polyornithine and laminin as previously described (Louis et al., Journal Of Pharmacology And Experimental Therapeutics, 262, 1274-1283, 1992).

The culture medium consisted of a 1:1 mixture of Dulbecco's Modified Eagle's Medium (DMEM) and F12 medium, and was supplemented with 2.5% heat-inactivated horse serum (Hyclone, Logan, UT), B27 medium supplement (GIBCO, Grand Island, NY), D-glucose (final concentration: 5mg/mL), L-glutamine (final concentration: 2mM), 20 mM HEPES, bovine insulin and human transferrin (final concentrations: 2.5 and 0.1 mg/mL, respectively).

10

Immunocytochemical identification of photoreceptors

Photoreceptors were identified by immunostaining for arrestin, a rod-specific antigen. Cultures of photoreceptors were fixed for 30 minutes at room temperature with 4% paraformaldehyde in PBS, pH 7.4, followed by three washes in PBS. The fixed cultures were then incubated in Superblock blocking buffer (Pierce, Rockford, IL), containing 1% Nonidet P-40 to increase the penetration of the antibodies. The anti-arrestin antibodies (polyclonal rabbit antibody against the synthetic peptide sequence of arrestin: Val-Phe-Glu-Glu-Phe-Ala-Arg-Gln-Asn-Leu-Lys-Cys) were then applied at a dilution of between 1:2000 in the same buffer, and the cultures were incubated for one hour at 37°C on a rotary shaker. After three washes with PBS, the cultures were incubated for one hour at 37°C with goat-anti-rabbit IgG (Vectastain kit from Vector Laboratories, Burlingame, CA) at a 1:500 dilution. After three washes with PBS, the secondary antibodies were then labeled with an avidin-biotin-peroxidase complex diluted at 1:500 (45 minutes at 37°C). After three more washes with PBS, the labeled cell cultures were reacted for 5-20 minutes in a solution of 0.1 M Tris-HCl, pH 7.4, containing 0.04% 3',3'-diaminobenzidine-(HCl)₄, 0.06 percent NiCl₂ and 0.02 percent hydrogen peroxide. Based on arrestin-immunoreactivity, about 90% of the cells in the cultures were rod photoreceptors.

The survival of photoreceptors was determined by examination of arrestin-stained cultures with bright-light optics at 200X magnification. The number of arrestin-positive photoreceptors was counted in one diametrical 1 X 6 mm strip, representing about 20 percent of the total surface area of a 6 mm-well. Viable photoreceptors were characterized as having a regularly-shaped cell body, with a usually short axon-like process. Photoreceptors showing signs of degeneration, such as having irregular, vacuolated perikarya or fragmented neurites, were excluded from the counts (most of the degenerating photoreceptors, however, detached from the culture substratum). Cell numbers were expressed either as cells/6-mm well.

Cultured rat retinal cells enriched for photoreceptors (10,000/6-mm well) were treated with human recombinant GDNF (ten-fold serial dilutions ranging from 10 ng/mL to 1 pg/mL). The cultures were fixed after six days and immunostained for arrestin, a rod photoreceptor-specific antigen. In cultures that were not treated with GDNF, the number of photoreceptors declined steadily over time to reach about 25 percent of the initial number after six days in culture. Treatment of the cultures with GDNF resulted in an about two-fold higher number of viable arrestin-positive photoreceptors after six days in culture. The effect of GDNF was maximal at about 200 pg/mL, with an ED₅₀ of about 30 pg/mL. In addition to promoting photoreceptor survival, the addition of the GDNF also stimulated the extension of their axon-like process, thereby demonstrating an effect on the morphological development of the photoreceptors (mean neurite length of photoreceptors in GDNF: 68 μ m, compared to 27 \pm 18 μ m in control cultures).

In order to confirm that rat retinal cells express high affinity GDNF receptors, [¹²⁵I]GDNF binding and photographic emulsion analysis were carried out. Post-natal rat photoreceptor cells were seeded on plastic slide flaskettes (Nunc) at a density of 2800 cells/mm², three to four days before the experiments. The cells were washed once with ice-cold washing buffer (Dulbecco's Modified Eagle's Medium (DMEM) containing 25 mM N-2-hydroxyethylpiperazine-N'-2-ethanesulfonic acid (HEPES), pH 7.5). For competitive binding, the cells were incubated with various concentrations of [¹²⁵I]GDNF in binding buffer (DMEM containing 25 mM HEPES, pH 7.5, and 2 mg/mL of bovine serum albumin (BSA)) in the presence or absence of 500 nM unlabeled GDNF at 4°C for four hours. Cells were washed four times with ice-cold washing buffer, lysed in 1 M NaOH and the radioactivity associated with the cells was determined in a gamma counter. A significant amount of [¹²⁵I]GDNF bound to the photoreceptor cells even at low ligand concentrations (as low as 30 pM), and this binding was inhibited completely by the presence of excess unlabeled GDNF.

For photographic emulsion detection, cells were incubated with 50 pM of [¹²⁵I]GDNF in binding buffer in the presence or absence of 500 nM unlabeled GDNF at 4°C for four hours. Cells were washed six times with ice-cold washing buffer, fixed with 2.5% glutaraldehyde and dehydrated sequentially with 50% and 70% ethanol, and dipped in NTB-2 photographic emulsion (Eastman Kodak, Rochester NY). After five days of exposure, the slides were developed and examined. The photographic emulsion analysis demonstrated the association of [¹²⁵I]GDNF to some of the photoreceptor cells, thereby indicating the presence of a

receptor for GDNF. This association, however, was efficiently blocked by the addition of unlabeled GDNF.

5

Example 2

Expression Cloning of a GDNFR- α from Photoreceptor Cells

Rat photoreceptor cells were selected as a possible source of a high affinity receptor for GDNF based upon their cell surface binding of radiolabeled GDNF and their ability to respond to very low concentrations of the ligand, as described in Example 1. In order to identify the receptor, a size-selected cDNA library of approximately 50,000 independent clones was constructed using a mammalian expression vector (a derivative of pSR, Takebe et al., 1988 supra) and mRNA isolated from cultured post-natal rat photoreceptor cells, by the methods described below. The library was divided into pools of approximately 1,500 to 2,000 independent clones and screened using an established expression cloning approach (Gearing et al., EMBO Journal, 8, 3667-3676, 1989). Plasmid DNA representing each pool of the library was prepared and transfected into COS7 cells grown on plastic microscope slide flaskettes (Nunc, Naperville, IL).

The transfected cells were treated with [125 I]GDNF, fixed with glutaraldehyde, dehydrated, and dipped in photographic emulsion for autoradiography. Following exposure for five days, the slides were developed and examined for the presence of cells covered by silver grains which indicated the binding of [125 I]GDNF to the cell surface as a result of the cell's expression of a receptor for GDNF. EGF receptor transfected cells treated with [125 I]EGF were used as a positive control.

One of the 27 pools (F8-11) screened in this manner exhibited 19 positive cells following transfection. Thus, a single cDNA library pool was identified which contained a cDNA clone that expressed GDNFR- α . This pool was divided into 60 smaller subpools of 100 clones/pool which were rescreened by the same procedure described above. Five of these pools were identified as positive and two of the five pools were further subdivided to yield single clones responsible for the GDNF binding activity. Transfection of plasmid DNA from the single clones into COS7 cells resulted in the binding of [125 I]GDNF to approximately 15% of the cells. This binding was specifically inhibited by competition with excess unlabeled GDNF.

Construction of Expression cDNA Libraries

Rat retinal cells were harvested from postnatal day 3-7 rats and seeded into culture dishes coated with laminin and polyornithine at a density of approximately 5700 cells/mm². After 3-4 days in culture, the population was estimated to contain approximately 80% photoreceptor cells. Total RNA was prepared from this culture by standard methods, and Poly A+ RNA was purified using a polyA-tract kit (Promega, Madison, WI). A cDNA library was constructed from the rat photoreceptor poly A+ RNA using the Gibco Superscript Choice System (Gibco/BRL, Gaithersburg, MD). Two micrograms of poly A+ RNA were mixed with 50 ng of random hexamers, heated to 70°C for 10 minutes and then quick-chilled on ice. First strand synthesis was carried out with 400U Superscript II RT at 37°C for one hour. Second strand synthesis was performed in the same tube after the addition of dNTPs, 10U of E. coli DNA ligase, 40U of E. coli DNA polymerase I, and 2U of E. coli RNase H. After two hours at 16°C, the cDNA ends were blunted by treatment with 10U of T4 polymerase for an additional five minutes at 16°C. Following isopropanol precipitation, EcoRI cloning sites were added to the cDNA by ligation overnight with 10 µg of unphosphorylated EcoRI adapter oligonucleotides.

The EcoRI adapted cDNA was then phosphorylated and applied to a Sephacryl S-500 HR size fractionation column. Following loading, the column was washed with 100 µl aliquots of TEN buffer (10 mM Tris-HCl pH 7.5, 0.1 mM EDTA, 25 mM NaCl), and 30 µl fractions were collected. Fractions 6 through 8, which contained approximately 34 ng of high molecular weight cDNA, were pooled and precipitated. The recovered EcoRI-adapted cDNA was ligated overnight with 50 ng of EcoRI cut vector pBJ5. Aliquots of the ligation mix containing about 15 ng cDNA each were transformed into competent cells (E. coli strain DH10B; GIBCO/BRL, Gaithersburg, MD) by electroporation. The transformation mixture was titered and then plated on 27 Amp/LB plates at a density of 1500 colonies/plate. Colonies were scraped from each plate and collected into 10 mL of Luria broth (LB) to make 27 pools of 1500 independent clones each. A portion of the cells from each pool was frozen in glycerol and the remainder was used to isolate plasmid DNA using a Qiagen tip-500 kit (Qiagen Inc., Chatsworth, CA).

COS Cell Transfection and Photographic Emulsion Analysis

COS7 cells were seeded (220,000 cells/slide) on plastic slide flaskettes (Nunc) coated with ProNectin (10 µg/mL in phosphate buffered saline (PBS)) one day before transfection. For transfection, 700 µl of Opti MEMI (GIBCO/BRL, Gaithersburg, MD) containing 2 µg cDNA was mixed gently with 35 µl of DEAE Dextran solution (10 mg/mL, Sigma, St. Louis, MO) in an Eppendorf tube. Cells

were washed twice with PBS and incubated with the transfection mix for 30 minutes at 37°C in a 5% CO₂ atmosphere. Following incubation, 3 mL of DMEM media containing 10% fetal calf serum (FCS) and 80 nM Chloroquine (Sigma, St. Louis, MO) were added to each flaskette. Cells were further incubated for 3.5 hours, shocked with 10% dimethylsulfoxide in DMEM at room temperature for two minutes, washed once with PBS, and allowed to grow in DMEM containing 10% FCS. After 48 hours, the transfected COS7 cells were washed once with ice-cold washing buffer (DMEM containing 25 mM HEPES, pH 7.5) and incubated in ice-cold binding buffer (DMEM containing 25 mM HEPES, pH 7.5 and 2 mg/mL BSA) supplemented with 50 pM [¹²⁵I]GDNF at 4°C for four hours. Cells were washed six times in ice-cold washing buffer, fixed with 2.5% glutaraldehyde at room temperature for five minutes, dehydrated sequentially with 50% and 70% ethanol, and then dipped in NTB-2 photographic emulsion (Eastman Kodak). After 4-5 day exposure at 4°C in dark, the slides were developed and screened by bright-field and dark-field microscopy.

Subdivision of Positive Pools

A single pool was identified which contained a putative GDNF receptor clone. Clones from this pool were plated on 60 plates at a density of 100 colonies/plate. Cells were scraped from each plate, collected in LB, and allowed to grow for 4-5 hours at 37°C. Frozen stocks and DNA preparations were made from each pool, as before, to generate 60 subpools containing 100 independent clones each. Two of these 60 subpools were identified as positive by the method described above, and clones from those pools were plated at low density to allow isolation of single colonies. Single colonies (384) were picked from each of the two subpools and grown for six hours in 200 µl LB in 96-well plates. In order to select single clones expressing GDNFR-α, the four 96-well plates were arrayed into a single large matrix consisting of 16 rows and 24 columns. Cells from the wells in each row and in each column were combined to yield a total of 40 mixtures. These mixtures were grown overnight in 10 mL LB/Amp (100 µg/mL), and DNA was prepared using a Qiagen tip-20 kit. When analyzed for putative GDNF receptor clones, three row mixtures and three column mixtures gave positive signals, suggesting nine potentially positive single clones. DNA from each of the potentially positive single clones was prepared and digested with EcoRI and PstI. DNA from three of the nine single clones exhibited identical restriction patterns while the other six were unrelated, suggesting that the three represented the authentic clones containing GDNFR-α.

Example 3
DNA Sequencing and Sequence Analysis

5

DNA from positive, single clones was prepared and sequenced using an automated ABI373A DNA sequencer (Perkin/Elmer Applied Biosystems, Santa Clara, CA) and dideoxy-dye-terminators, according to manufacturer's instructions. Comparison of GDNFR- α sequence with all available public databases was performed using the FASTA (Pearson and Lipman, Proceedings Of The National Academy Of Sciences U.S.A., 85, 2444-2448, 1988) program algorithm as described in the University of Wisconsin Genetics Computer Group package (Program Manual for the Wisconsin Package, Version 8, September 1994, Genetics Computer Group, Madison, WI).

15

Sequence Characterization of the Rat GDNFR- α

Plasmid DNA from the clones described in Example 2, above, was prepared and submitted for DNA sequence analysis. Nucleotide sequence analysis of the cloned 2138 bp rat cDNA revealed a single large open reading frame encoding a translation protein of 468 amino acid residues (Figure 3).

20

The coding sequence is flanked by a 5'-untranslated region of 301 bp and a 3'-untranslated region of 430 bp that does not contain a potential polyadenylation site. The presence of an in-frame stop codon upstream of the first ATG at base pair 302 and its surrounding nucleotide context indicate that this methionine codon is the most likely translation initiator site (Kozak, Nucleic Acids Research. 15, 8125-8148, 1987).

25

No polyadenylation signal is found in the 430 nucleotides of 3' untranslated sequence in the rat cDNA clone. This is not surprising, since the Northern blot data shows the shortest mRNA transcripts to be approximately 3.6 kb.

30

The GDNFR- α polypeptide sequence has an N-terminal hydrophobic region of approximately 19 residues (methionine-1 to alanine-19, Figure 3) with the characteristics of a secretory signal peptide (von Heijne, Protein Sequences And Data Analysis. 1, 41-42, 1987; von Heijne, Nucleic Acids Research. 14, 4683-4690, 1986). No internal hydrophobic domain that could serve as a transmembrane domain was found. Instead, a carboxy-terminal hydrophobic region of 21 residues (leucine-448 to serine-468 in Figure 3) is present and may be involved in a glycosyl-phosphatidylinositol (GPI) anchorage of the receptor to the cytoplasmic membrane.

35

Except for the presence of three potential N-linked glycosylation sites, no conserved sequence or structural motifs were found. The protein is extremely rich in cysteine (31 of the 468 amino acid residues) but their spacing is not shared with that of cysteine-rich domains found in the extracellular portions of known receptors.

5 The GDNFR- α sequence was compared to sequences in available public databases using FASTA. The search did not reveal significant homology to other published sequences. Once the rat cDNA clone was obtained, it was radiolabeled and used to probe a cDNA library prepared from human brain substantia nigra as described below in Example 5.

10

Example 4

GDNF Binding to Cells Expressing GDNFR- α

15 A binding assay was performed in accordance with an assay method previously described by Jing et al.. (Journal Of Cell Biology, 110, 283-294, 1990). The assay involved the binding of [125 I]GDNF to rat photoreceptor cells, COS7 cells or 293T cells which had been transfected to express GDNFR- α . Recombinant GDNFR- α expressed on the surface of 293T cells was able to bind GDNF
20 specifically and with an affinity comparable to that observed for GDNF binding sites on rat retinal cells.

Rat photoreceptor cells were prepared as described in Example 1, above, and seeded at a density of 5.7×10^5 cells/cm² two to three days before the assay in 24-well Costar tissue culture plates pre-coated with polyornithine and laminin. COS7
25 cells were seeded at a density of 2.5×10^4 cells/cm² one day before the assay and transfected with 10-20 μ g of plasmid DNA using the DEAE-dextran-chloroquine method (Aruffo and Seed, Proceedings Of The National Academy Of Sciences U.S.A., 84, 8573-8577, 1987). Cells from each dish were removed and reseeded into 30 wells of 24-well Costar tissue culture plates 24 hours following the transfection,
30 and allowed to grow for an additional 48 hours. Cells were then left on ice for 5 to 10 minutes, washed once with ice-cold washing buffer and incubated with 0.2 mL of binding buffer containing various concentrations of [125 I]GDNF with or without unlabeled GDNF at 4°C for four hours. Cells were washed four times with 0.5 mL ice-cold washing buffer and lysed with 0.5 mL of 1 M NaOH. The lysates were
35 counted in a 1470 Wizard Automatic Gamma Counter.

For some binding experiments, transiently transfected 293T cells were used (see below for 293T cell transfection). Two days following transfection, cells were

removed from dishes by 2x versine. Cells were pelleted, washed once with ice-cold binding buffer and resuspended in ice-cold binding buffer at a density of 3×10^5 cells/mL. The cell suspension was divided into aliquots containing 1.5×10^5 cell/sample. Cells were then pelleted and incubated with various concentrations of $[^{125}\text{I}]\text{GDNF}$ in the presence or absence of 500 nM of unlabeled GDNF at 4°C for four hours with gentle agitation. Cells were washed four times with ice-cold washing buffer and resuspended in 0.5 mL washing buffer. Two 0.2 mL aliquots of the suspension were counted in a gamma counter to determine the amount of $[^{125}\text{I}]\text{GDNF}$ associated with the cells.

In all assays, nonspecific binding was determined by using duplicate samples, one of which contained 500 nM of unlabeled GDNF. The level of nonspecific binding varied from 10% to 20% of the specific binding measured in the absence of unlabeled GDNF and was subtracted from the specific binding. The assays demonstrated that cells did not bind GDNF unless the cell had been transfected with the GDNFR- α cDNA clone.

Example 5

Tissue Distribution of GDNFR- α mRNA

The pattern of expression of GDNFR- α mRNA in embryonic mouse, adult mouse, rat, and human tissues was examined by Northern blot analysis. The cloned rat GDNFR- α cDNA was labeled using the Random Primed DNA Labeling Kit (Boehringer Mannheim, Indianapolis, IN) according to the manufacturer's procedures. Rat, mouse, and human tissue RNA blots (purchased from Clontech, Palo Alto, CA) were hybridized with the probe and washed using the reagents of the ExpressHyb Kit (Clontech) according to the manufacturer's instructions.

Tissue Northern blots prepared from adult rat, mouse, and human tissues indicated that GDNFR- α mRNA is most highly expressed in liver, brain, and kidney. High mRNA expression was also detected in lung, with lower or non-detectable amounts in spleen, intestine, testis, and skeletal muscle. In blots made from mRNA isolated from mouse embryo, expression was undetectable at embryonic day 7, became apparent at day E11, and was very high by day E17. GDNFR- α mRNA was expressed in tissue isolated from several subregions of adult human brain at relatively equal levels. Expression of GDNFR- α mRNA in human adult brain showed little specificity for any particular region.

In most tissues, transcripts of two distinct sizes were present. In mouse and

human tissues, transcripts of 8.5 and 4.4 kb were found, while in rat the transcripts were 8.5 and 3.6 kb. The relative amounts of the larger and smaller transcripts varied with tissue type, the smaller transcript being predominant in liver and kidney and the larger being more abundant in brain. The binding of GDNF to 293T cells transfected with a GDNFR- α cDNA clone in the pBKRSV vector was examined by Scatchard analysis. Two classes of binding sites were detected, one with a binding affinity in the low picomolar range and another with an affinity of about 500 pM.

10

Example 6

Recombinant Human GDNFR- α

An adult human substantia nigra cDNA library (5'-stretch plus cDNA library, Clontech, Palo Alto, CA) cloned in bacteriophage gt10 was screened using the rat GDNFR- α cDNA clone of Example 1 as a probe. The probe was labeled with [^{32}P]-dNTPs using a Random Primed DNA Labeling Kit (Boehringer Mannheim, Indianapolis, IN) according to the manufacturer's instructions. Approximately 1.2×10^6 gt10 phage from the human substantia nigra cDNA library were plated on 15 cm agarose plates and replicated on duplicate nitrocellulose filters. The filters were then screened by hybridization with the radiolabeled probe. The filters were prehybridized in 200 mL of 6 x SSC, 1 x Denhardt's, 0.5% SDS, 50 $\mu\text{g/mL}$ salmon sperm DNA at 55°C for 3.5 hours. Following the addition of 2×10^8 cpm of the radiolabeled probe, hybridization was continued for 18 hours. Filters were then washed twice for 30 minutes each in 0.5x SSC, 0.1% SDS at 55°C and exposed to X-ray film overnight with an intensifying screen.

Five positive plaques were isolated whose cDNA inserts represented portions of the human GDNFR- α cDNA. In comparison to the nucleic acid sequence of rat GDNFR- α depicted in Figure 3 (bp 0 through 2140), the five human GDNFR- α clones were found to contain the following sequences:

30

TABLE 3

Clone 2	1247 through 2330 (SEQ ID NO:21)
Clone 9	1270 through 2330 (SEQ ID NO:23)
Clone 21-A	-235 through 1692 (SEQ ID NO:9)
Clone 21-B	-237 through 1692 (SEQ ID NO:11)
Clone 29	805 through 2971 (SEQ ID NO:15)

An alignment and comparison of the sequences, as depicted in Figure 5, provided a consensus sequence for human GDNFR- α . The translation product predicted by the human cDNA sequence consists of 465 amino acids and is 93% identical to rat GDNFR- α .

To generate a human cDNA encoding the full length GDNFR- α , portions of clones 21B and 2 were spliced together at an internal BglII site and subcloned into the mammalian expression vector pBKRSV (Stratagene, La Jolla, CA).

Recombinant human GDNFR expression vectors may be prepared for expression in mammalian cells. As indicated above, expression may also be in non-mammalian cells, such as bacterial cells. The nucleic acid sequences disclosed herein may be placed into a commercially available mammalian vector (for example, CEP4, Invitrogen) for expression in mammalian cells, including the commercially available human embryonic kidney cell line, "293". For expression in bacterial cells, one would typically eliminate that portion encoding the leader sequence (e.g., nucleic acids 1-590 of Figure 1). One may add an additional methionyl at the N-terminus for bacterial expression. Additionally, one may substitute the native leader sequence with a different leader sequence, or other sequence for cleavage for ease of expression.

Example 7 Soluble GDNFR Constructs

Soluble human GDNFR protein products were made. The following examples provide four different forms, differing only at the carboxy terminus, indicated by residue numbering as provided in Figure 2. Two are soluble forms truncated at different points just upstream from the hydrophobic tail and downstream from the last cysteine residue. The other two are the same truncations but with the addition of the "FLAG" sequence, an octapeptide to which a commercial antibody is available (Eastman Kodak). The FLAG sequence is H₂N- DYKDDDDK - COOH.

Method

Lambda phage clone #21, containing nearly the entire coding region of human GDNFR- α , was digested with EcoRI to excise the cDNA insert. This fragment was purified and ligated into EcoRI cut pBKRSV vector (Stratagene, La Jolla, CA) to produce the clone 21-B-3/pBKRSV. Primers 1 and 2 as shown below

were used in a PCR reaction with the human GDNFR- α clone 21-B-3/pBKRSV as template. PCR conditions were 94°C, five minutes followed by 25 cycles of 94°C, one minute; 55°C, one minute; 72°C, two minutes and a final extension of five minutes at 72°C. This produced a fragment consisting of nucleotides 1265-1868 of the human GDNFR- α clone plus a termination codon and Hind III restriction site provided by primer 2. This fragment was digested with restriction enzymes Hind III (contained in primer 2) and BglII (position 1304 in human GDNFR- α), and the resulting 572 nucleotide fragment was isolated by gel electrophoresis. This fragment contained the hGDNFR- α - coding region from isoleucine-255 to glycine-443. A similar strategy was used with primers 1 and 3 to produce a fragment with BglII and HindIII ends which coded for isoleucine-255 to proline-446. Primers 4 and 5 were designed to produce fragments coding for the same regions of hGDNFR- α and primers 1 and 3, but with the addition of the Flag peptide coding sequence (IBI/Kodak, New Haven, CN). The Flag peptide sequence consists of eight amino acids (H2N-Asp-Tyr-Lys-Asp-Asp-Asp-Lys-COOH) to which antibodies are commercially available. Primers 1 and 4 or 1 and 5 were used in PCR reactions with the same template as before, and digested with HindIII and BglII as before. This procedure produced fragments coding for isoleucine-255 to glycine-443 and isoleucine-255 to proline-446, but with the addition of the Flag peptide at their carboxy termini.

Primers

- 1) 5'-CTGTTTGAATTTGCAGGACTC-3' (SEQ ID NO:30)
- 2) 5'-CTCCTCTCTAAGCTTCTAACCACAGCTTGGAGGAGC-3' (SEQ ID NO:31)
- 3) 5'-CTCCTCTCTAAGCTTCTATGGGCTCAGACCACAGCTT-3' (SEQ ID NO:32)
- 4) 5'-CTCCTCTCTAAGCTTCTACTTGTTCATCGTCGTCCTTGTAGTCACCACAGCTTGGAGGAGC-3' (SEQ ID NO:33)
- 5) 5'-CTCCTCTCTAAGCTTCTACTTGTTCATCGTCGTCCTTGTAGTCTGGCTCAGACCACAGCTT-3' (SEQ ID NO:34)

30

All four fragments, produced as described above, were transferred back into 21B3/pBKRSV. The 21B3/pBKRSV clone was digested with BglII and HindIII, and treated with calf intestinal alkaline phosphatase (CIAP). The large fragment containing the vector and the human GDNFR- α coding region up to the BglII site was gel purified and extracted from gel. Each of the four BglII/HindIII fragments produced as described above were ligated into this vector resulting in the following constructs in the pBKRSV vector:

35

TABLE 4

- | | |
|---|--|
| 1) GDNFR- α /gly-443/pBKRSV | hGDNFR- α terminating at glycine 443,
followed by stop codon |
| 2) GDNFR- α /pro-446/pBKRSV | hGDNFR- α terminating at proline 446,
followed by stop codon |
| 3) GDNFR- α /gly-443/Flag/pBKRSV | hGDNFR- α terminating at glycine 443 with C-term Flag tag, followed by stop codon |
| 4) GDNFR- α /pro-446/Flag/pBKRSV | hGDNFR- α terminating at proline 446 with C-term Flag tag, followed by stop codon |

5 Correct construction of all clones was confirmed by DNA sequencing. Inserts from the pBKRSV clones were transferred to other expression vectors using enzyme sites present in the pBKRSV polylinker sequence as described below. Soluble GDNFRs (e.g., sGDNFR- α /gly and sGDNFR- α /pro) have also been transferred into vectors for transient expression and into pDSR-2 for stable
10 expression in CHO cells.

pDSR α 2+PL clones:

The appropriate pBKRSV clone is digested with XbaI and SalI. The insert is ligated to pDSR α 2+PL cut with the same enzymes and treated with CIAP. This
15 construction may be used for stable expression of GDNFR in CHO cells.

pCEP4 clones:

The appropriate pBKRSV clone is digested with SpeI and XhoI. The insert is ligated to pCEP4 (Invitrogen, San Diego, CA) digested with NheI (SpeI ends) and
20 XhoI, and treated with CIAP. This construction may be used for transient of expression of GDNFR.

The plasmid construct pDSR-2 is prepared substantially in accordance with the process described in the co-owned and copending U. S. Patent Application Serial
25 Number 501,904 filed March 29, 1990 (also see, European Patent Application No. 90305433, Publication No. EP 398 753, filed May 18, 1990 and WO 90/14363 (1990), the disclosures of which are hereby incorporated by reference. It will be appreciated by those skilled in the art that a variety of nucleic acid sequences encoding GDNFR analogs may be used.

Another construct is pDSR α 2, a derivative of the plasmid pCD (Okayama & Berg, Mol. Cell Biol. 3: 280-289, 1983) with three main modifications: (i) the SV40 polyadenylation signal has been replaced with the signal from the α -subunit of bovine follicular stimulating hormone, α -bFSH (Goodwin et al., Nucleic Acids Res. 11: 6873-6882, 1983); (ii) a mouse dihydrofolate reductase minigene (Gasser et al., Proc. Natl. Acad. Sci. 79: 6522-6526, 1982) has been inserted downstream from the expression cassette to allow selection and amplification of the transformants; and (iii) a 267 bp fragment containing the "R-element" and part of the "U5" sequences of the long terminal repeat (LTR) of human T-cell leukemia virus type I (HTLV-I) has been cloned and inserted between the SV40 promoter and the splice signals as described previously (Takebe et al., Mol. Cell Biol. 8: 466-472, 1988).

The expression of GDNFR- α in CHO cells has been verified by the binding of iodinated GDNF to the cell surface. As discussed above, the recombinantly expressed soluble GDNFR- α protein product may be used to potentiate the activity or cell specificity of GDNF. Soluble GDNFR- α attached to a detectable label also may be used in diagnostic applications as discussed above.

Example 8

Chemical Crosslinking of GDNF with GDNFR- α

In order to study its binding properties and molecular characteristics, GDNFR- α was transiently expressed on the surface of 293T cells by transfection of the rat cDNA clone. Transfection of 293T cells was performed using the Calcium Phosphate Transfection System (GIBCO/BRL, Gaithersburg, MD) according to the manufacturers instructions. Two days following transfection, cells were removed by 2x versine treatment, washed once with washing buffer, and resuspended in washing buffer at a density of 2×10^6 cells/mL. A duplicate set of cells were incubated with 0.5 u/mL PI-PLC at 37°C for 30 minutes before [125 I]GDNF binding. These cells were washed three times with ice-cold binding buffer and then incubated with 1 to 3 nM of [125 I]GDNF along with other cells at 4°C for four hours. Cells were washed four times with ice-cold washing buffer, resuspended in washing buffer supplemented with 1 mM of Bis suberate for crosslinking (BS³ Pierce, Rockford, IL) and incubated at room temperature for 30 minutes. Following three washes with TBS, a duplicate group of samples was treated by 0.5 u/mL of PI-PLC at 37°C for 30 minutes. These cells were pelleted and the supernatants were collected. The cells were then washed with washing buffer and lysed along with all other cells with 2x

SDS-PAGE sample buffer. The cell lysates and the collected supernatants were resolved on a 7.5% SDS-PAGE.

The cell suspension was divided into aliquots containing 1.5×10^5 cell/sample. Cells were then pelleted and incubated with various concentrations of [125 I]GDNF in the presence or absence of 500 nM of unlabeled GDNF at 4°C for four hours with gentle agitation. Cells were washed four times with ice-cold washing buffer and resuspended in 0.5 mL washing buffer. Two 0.2 mL aliquots of the suspension were counted in a gamma counter to determine the amount of [125 I]GDNF associated with the cells.

Although mock transfected 293T cells did not exhibit any GDNF binding capacity, GDNFR- α transfected cells bound [125 I]GDNF strongly even at picomolar concentrations. This binding was almost completely inhibited by 500 nM of unlabeled GDNF, indicating a specific binding of native GDNF to the expressed receptors.

GDNFR- α expressed by the 293T cells can be released from the cells by treatment with phosphatidylinositol-specific phospholipase C (PI-PLC, Boehringer Mannheim, Indianapolis, IN). The treatment of transfected cells with PI-PLC prior to ligand binding almost entirely eliminated the GDNF binding capacity of the cell. Additionally, treatment of the transfected cells after cross-linking released the majority of the cross-linked products into the media. These results strongly suggest that GDNFR- α is anchored to the cell membrane through a GPI linkage.

Crosslinking data further indicated that the molecular weight of GDNFR- α is approximately 50-65 kD, suggesting that there is a low level of glycosylation. Although the major cross-linked species has a molecular mass consistent with a monomer of the receptor, a minor species with approximately the mass expected for a dimer has been found.

Example 9

GDNF Signaling is Mediated by a Complex of GDNFR- α and the Ret Receptor Protein Tyrosine Kinase

Introduction

Mice carrying targeted null mutations in the GDNF gene exhibit various defects in tissues derived from neural crest cells, in the autonomic nervous system, and in trigeminal and spinal cord motor neurons. The most severe defects are the

absence of kidneys and complete loss of enteric neurons in digestive tract. The phenotype of GDNF knockout mice is strikingly similar to that of the c-ret knockout animals (Schuchardt et al. 1994), suggesting a possible linkage between the signal transduction pathways of GDNF and c-ret.

5 The proto-oncogene c-ret was identified using probes derived from an oncogene isolated in gene transfer experiments (Takahashi et al., Cell. 42, 581-588, 1985; Takahashi and Cooper, Mol. Cell. Biol., 7, 1378-1385, 1987). Sequence analysis of the c-ret cDNA revealed a large open reading frame encoding a novel
10 receptor protein tyrosine kinase (PTK). The family of receptor PTKs has been grouped into sub-families according to extracellular domain structure and sequence homology within the intracellular kinase domain (van der Geer et al., 1994). The unique extracellular domain structure of Ret places it outside any other known receptor PTK sub-family; it includes a signal peptide, a cadherin-like motif, and a cysteine-rich region (van Heyningen, Nature, 367, 319-320, 1994; Iwamoto et al.,
15 1993). *In situ* hybridization and immunohistochemical analysis showed high level expression of ret mRNA and protein in the developing central and peripheral nervous systems and in the excretory system of the mouse embryo (Pachnis et al., 1993; Tsuzuki et al., Oncogene, 10, 191-198, 1995), suggesting a role of the Ret receptor either in the development or in the function of these tissues. A functional
20 ligand of the Ret receptor has not been identified, thereby limiting a further understanding of the molecular mechanism of Ret signaling.

 Mutations in the c-ret gene are associated with inherited predisposition to cancer in familial medullary thyroid carcinoma (FMTC), and multiple endocrine neoplasia type 2A (MEN2A) and 2B (MEN2B). These diseases are probably caused
25 by "gain of function" mutations that constitutively activate the Ret kinase (Donis-Keller et al., Hum. Molec. Genet. 2, 851-856, 1993; Hofstra et al., Nature. 367, 375-376, 1994; Mulligan et al., Nature. 363, 458-460, 1993; Santoro et al., Science. 267, 381-383, 1995). They confer a predisposition to malignancy specifically in tissues derived from the neural crest, where ret is normally expressed in early
30 development. Another ret-associated genetic disorder, Hirschsprung's disease (HSCR), is characterized by the congenital absence of parasympathetic innervation in the lower intestinal tract (Edery et al., Nature. 367, 378-380, 1994; Romeo et al., 1994). The most likely causes of HSCR are nonsense mutations that result in the production of truncated Ret protein lacking a kinase domain or missense mutations
35 that inactivate the Ret kinase. As noted above, targeted disruption of the c-ret proto-oncogene in mice results in renal agenesis or severe dysgenesis and lack of enteric neurons throughout the digestive tract (Schuchardt et al., 1994). This phenotype

closely resembles that of GDNF knockout mice. Taken together, these data suggest that both Ret and GDNF are involved in signal transduction pathways critical to the development of the kidney and the enteric nervous system. How Ret and GDNF are involved, however, was not known.

5 The isolation and characterization of cDNA for GDNFR- α by expression cloning, as described above, lead to the expression of GDNFR- α in the transformed human embryonic kidney cell line 293T. Transformation resulted in the appearance of both high (K_d of approximately 2 pM) and low (K_d of approximately 200 pM) affinity binding sites. The high affinity binding sites could be composed of
10 homodimers or homo-oligomers of GDNFR- α alone, or of heterodimers or hetero-oligomers of GDNFR- α with other molecules. As discussed above, because GDNFR- α lacks a cytoplasmic domain, it must function through one or more accessory molecules in order to play a role in GDNF signal transduction. In this study we confirm that, in the presence of GDNFR- α , GDNF associates with the Ret
15 protein tyrosine kinase receptor, and quickly induces Ret autophosphorylation.

Results

Neuro-2a Cells Expressing GDNFR- α Bind GDNF with High Affinity

20 Neuro-2a is a mouse neuroblastoma cell line that endogenously expresses a high level of Ret protein (Ikeda et al., Oncogene. 5, 1291-1296, 1990; Iwamoto et al., Oncogene. 8, 1087-1091, 1993; Takahashi and Cooper, 1987) but does not express detectable levels of GDNFR- α mRNA as judged by Northern blot. In order to determine if Ret could associate with GDNF in the presence of GDNFR- α , a study
25 was performed to examine the binding of [125 I]GDNF to Neuro-2a cells engineered to express GDNFR- α . Neuro-2a cells were transfected with a mammalian expression vector containing the rat GDNFR- α cDNA (such as the expression plasmid described above). Three clonal lines, NGR-16, NGR-33, and NGR-38 were tested for their ability to bind [125 I]GDNF. The unbound [125 I]GDNF was
30 removed at the end of the incubation and the amount of radioactivity associated with the cells was determined as described in Experimental Procedures. All three lines were able to bind [125 I]GDNF specifically while parental Neuro-2a cells exhibited little or no [125 I]GDNF binding (Figure 6). Binding could be effectively competed by the addition of 500 nM unlabeled GDNF. These results demonstrate that Ret
35 receptor expressed on Neuro-2a cells is unable to bind GDNF in the absence of GDNFR- α and are consistent with the previous observation that GDNFR- α is not expressed at appreciable levels in Neuro-2a cells.

Equilibrium binding of [125 I]GDNF to NGR-38 cells was examined over a wide range of ligand concentrations (0.5 pM to 1 nM of [125 I]GDNF in the presence or absence of 500 nM of unlabeled GDNF) (see Figure 7A). Following incubation, unbound [125 I]GDNF was removed and the radioactivity associated with the cells was determined as described in Experimental Procedures. Results are depicted in Figure 7: (A) Equilibrium binding of [125 I]GDNF to NGR-38 cells (circles) and Neuro-2a cells (squares) in the presence (open circles and open squares) or absence (filled circles and filled squares) of unlabeled GDNF; (B) Scatchard analysis of [125 I]GDNF binding to NGR-38 cells. Neuro-2a cells exhibited little binding even at a concentration of 1 nM [125 I]GDNF, and this binding was not affected by the addition of excess unlabeled GDNF. Binding to NGR-38 cells was analyzed by Scatchard plot as shown in Figure 7B. Two classes of binding sites were detected, one with $K_d = 1.5 \pm 0.5$ pM and the other with $K_d = 332 \pm 53$ pM. These dissociation constants are very similar to the values obtained for the high and low affinity binding sites in 293T cells transiently expressing GDNFR- α , as described above.

GDNF Associates with Ret in Neuro-2a Cells Expressing GDNFR- α

In order to determine if the Ret receptor PTK could associate with GDNF in cells expressing GDNFR- α , a cross-linking experiment was carried out using NGR-38 and parental Neuro-2a cells. NGR-38 cells were incubated with [125 I]GDNF, treated with cross-linking reagent, then lysed either directly in SDS-PAGE sample buffer or in Triton X-100 lysis buffer and further immunoprecipitated with anti-Ret antibody as described in the Experimental Procedures. The immunoprecipitates were analyzed by SDS-PAGE in the absence (NR) or presence (R) of -mercaptoethanol. Lysates were treated with Ret specific antibody, immunoprecipitated, and analyzed by SDS-PAGE under reducing conditions (see Figure 8, bands are marked as follows: ~75 kD, solid triangle; ~150 kD, open triangle; ~185 kD, solid arrow; ~250 kD, asterisk; ~400kD, open arrow). The most prominent cross-linked species were at ~75 kD, and ~185 kD, with less intense bands of ~150 kD and ~250 kD. A very faint band of ~400 kD was also visible (Figure 8, lane 2). When immunoprecipitates were analyzed by non-reducing SDS-PAGE, the ~75 kD, ~150 and ~185 kD bands were present at about the same intensity as in the reducing gel, but the amount of the ~400 kD band increased dramatically (Figure 8, lane 4). Also becoming more prominent was the band at ~250 kD.

Under both reducing and non-reducing conditions, bands of similar

molecular weight but of greatly reduced intensity were observed when parental Neuro-2a cells were used instead of NGR-38 (Figure 8, lanes 1 and 3). The ~75 kD and ~150 kD species are likely to represent cross-linked complexes of GDNF and GDNFR- α , since species with identical molecular weights are produced by cross-linking in 293T cells that do not express Ret. Furthermore, since the molecular weight of Ret is 170 kD, any complex including Ret must be of at least this size.

The fact that these complexes are immunoprecipitated by anti-Ret antibody indicates they are products of an association between Ret and the GDNF/GDNFR- α complex which was disrupted under the conditions of the gel analysis. It is envisioned that the broad band at ~185 kD probably consists of one molecule of Ret (170 kD) cross-linked with one molecule of monomeric recombinant GDNF (15 kD), although some dimeric GDNF may be included. The presence of Ret in this species was confirmed by a separate experiment in which a band of the same molecular weight was observed when unlabeled GDNF was cross-linked to NGR-38 cells and the products examined by Western blot with anti-Ret antibody (data not shown).

The ~400 kD band was not reliably identified, partly due to the difficulty in estimating its molecular weight. The fact that it is prominent only under non-reducing conditions indicates that it is a disulfide-linked dimer of one or more of the species observed under reducing conditions. The most likely explanation is that it represents a dimer of the 185 kD species, although it may be a mixture of high molecular weight complexes consisting of two Ret, one or two GDNFR- α , and one or two GDNF molecules. The exact identity of the ~250 kD band has not yet been determined. One possibility is that it represents cross-linked heterodimers of the ~75 kD (GDNF + GDNFR- α) and ~185 kD (GDNF + Ret) complexes.

GDNF Stimulates Autophosphorylation of Ret in Neuro-2a Cells Expressing GDNFR- α

The ability of the Ret protein tyrosine kinase receptor to associate with GDNF in the presence of GDNFR- α led to the study of GDNF stimulation of the autophosphorylation of Ret. NGR-38 cells were treated with GDNF, lysed, and the lysates immunoprecipitated with anti-Ret antibody. The immunoprecipitates were analyzed by Western blot using an anti-phosphotyrosine antibody as described in the Experimental Procedures. When NGR-38 cells (Figure 9A, lanes 2-4) were treated with purified recombinant GDNF produced in either mammalian (CHO cells; Figure 9A, lanes 4) or E. coli cells (Figure 9A, lanes 1, 3), a strong band was observed at 170 kD, indicating autophosphorylation of tyrosine residues on the

mature form of Ret. A much weaker corresponding band was observed in GDNF-treated Neuro-2a cells (Figure 9A, lane 1). No phosphorylation was observed on the alternatively glycosylated 150 kD precursor form of Ret (Figure 9A). The induction of Ret autophosphorylation by GDNF was dosage dependent. The dose response and kinetics of GDNF-induced Ret tyrosine phosphorylation in NGR-38 cells are shown in panels B and C. In all panels, the tyrosine phosphorylated 170 kD Ret bands are indicated by solid arrows. The amount of Ret protein loaded in each lane as determined by reprobing of the immunoblot with anti-Ret antibody (Santa Cruz, C-19, Cat. #sc-167) is shown on the right side of panel A. The band at ~150 kD represents an alternately glycosylated immature form of Ret that does not autophosphorylate. As shown in Figure 9B, stimulation of Ret autophosphorylation in NGR-38 cells could be detected with 50 pg/mL of GDNF and the response was saturated at 20-50 ng/mL GDNF. The stimulation of Ret autophosphorylation by purified recombinant GDNF in NGR-38 cells over times of 0-20 minutes following treatment is shown in Figure 9C. Increased levels of Ret autophosphorylation could be observed within one minute of GDNF treatment and was maximal at 10 minutes following treatment (Figure 9C).

GDNF and Soluble GDNFR- α Induce Ret Autophosphorylation in Neuro-2A Cells

As discussed above, GDNFR- α is anchored to the cytoplasmic membrane through a GPI linkage and can be released by treatment with phosphatidylinositol-specific phospholipase C (PI-PLC). When NGR-38 cells were incubated with PI-PLC, GDNF-induced receptor autophosphorylation of Ret in these cells was abolished (Figure 10A; PI-PLC treated (lane 1) or untreated (lanes 2 and 3) NGR-38 cells were incubated with (lanes 1 and 3) or without (lane 2) GDNF and analyzed for Ret autophosphorylation by immunoblotting as described in the Experimental Procedures).

Figure 10B depicts parental Neuro-2a cells treated with (lanes 2,4,6,8) or without (lanes 1,3,5,7) GDNF in the presence (lanes 5-8) or absence (lanes 1-4) of PI-PLC/CM obtained from Neuro-2a or NGR-38 cells, as analyzed for Ret autophosphorylation by immunoblotting as described in the Experimental Procedures. NGR-38 cells treated with GDNF were used as a positive control. In both panels A and B, the autophosphorylated 170 kD Ret bands are marked by solid arrows. When conditioned medium containing soluble GDNFR- α released by PI-PLC treatment (PI-PLC/CM) of NGR-38 cells was added to parental Neuro-2a cells along with GDNF, autophosphorylation of the Ret receptor comparable to that obtained with GDNF treatment of NGR-38 cells was observed (Figure 10B, lanes 2

and 8). Only background levels of Ret autophosphorylation were observed when no GDNF was added, or when conditioned media derived from PI-PLC treatment of Neuro-2a cells was tested (Figure 10B, lanes 3-7).

5 Ret-Fc Fusion Protein Blocks Ret Phosphorylation Induced by GDNF and Soluble GDNFR- α

To confirm that Ret phosphorylation induced by GDNF in the presence of GDNFR- α is the result of receptor autophosphorylation, a study was performed to determine whether a Ret extracellular domain/Immunoglobulin Fc (Ret-Fc) fusion protein could block Ret activation. Because of the technical difficulty of blocking the large number of GDNF alpha receptors expressed on NGR-38 cells, Ret phosphorylation assays were performed using Neuro-2a as the target cell and culture media removed from NGR-38 cells treated with PI-PLC as a source of GDNFR- α . Cells were treated with mixtures including various combinations of GDNF (50 ng/mL), media containing soluble GDNFR- α (e.g., PI-PLC/CM derived from NGR-38 cells), and different concentrations of Ret-Fc fusion protein either alone or in various combinations as indicated in Figure 11. Neuro-2a cells were treated with GDNF, media containing soluble GDNFR- α , Ret-Fc, or the pre-incubated mixtures. The cells were then lysed, and the lysates were analyzed for c-Ret autophosphorylation by immunoprecipitation using anti-Ret antibody as described in the Experimental Procedures. The immunoprecipitates were analyzed by Western blot using an anti-phosphotyrosine antibody.

The pre-incubated mixture of GDNF and media containing soluble GDNFR- α induced tyrosine phosphorylation of Ret receptors expressed in Neuro-2a at a level comparable to GDNF-treated NGR-38 control cells (Figure 11, lanes 7 and 2). The position of the autophosphorylated 170 kD Ret bands are marked by a solid arrow. When Ret-Fc fusion protein was included in the pre-incubated GDNF/GDNFR- α mixture, Ret phosphorylation was inhibited in a dose dependent manner (Figure 11, lanes 8-10). This indicated that Ret phosphorylation is a result of a GDNF/Ret interaction mediated by GDNFR- α . In untreated Neuro-2a cells or in cells treated with any combination of GDNF or Ret-Fc fusion protein in the absence of GDNFR- α , only background levels of Ret phosphorylation were observed (Figure 11, lanes 3-6).

35 GDNF Induces Autophosphorylation of c-RET Expressed in Embryonic Motor Neurons

Spinal cord motor neurons are one of the major targets of GDNF action in

vivo (Henderson et al., Science. 266, 1062-1064, 1994; Li et al., Proceedings Of The National Academy Of Sciences, U.S.A. 92, 9771-9775, 1995; Oppenheim et al., Nature. 373, 344-346, 1995; Yan et al., Nature. 373, 341-344, 1995; Zurn et al., Neuroreport. 6, 113-118, 1995). To test the ability of GDNF to induce Ret autophosphorylation in these cells, embryonic rat spinal cord motor neurons were treated with (lanes 2 and 4) or without (lanes 1 and 3) 20 ng/mL GDNF followed by lysis of the cells, immunoprecipitation with anti-Ret antibody, and analysis by Western blotting with anti-phosphotyrosine antibody as described in the Experimental Procedures. In lysates of cells treated with GDNF, a band of tyrosine phosphorylated protein with a molecular mass of ~170 kD was observed (Figure 12, lane 2). No such signal was observed with cells treated with binding buffer alone (Figure 12, lane 1). When the same Western blot filter was stripped and re-probed with anti-Ret antibody (i.e., the amount of c-Ret protein loaded in each lane was determined by reprobing the immunoblot with the anti-Ret antibody), bands with the same molecular mass and similar intensities appeared in both samples (Figure 12, lanes 3 and 4). The phosphotyrosine band in GDNF-treated cells co-migrates with the Ret protein band, indicating GDNF stimulated autophosphorylation of Ret. The autophosphorylated Ret bands (lanes 1 and 2) and the corresponding protein bands (lanes 3 and 4) were marked by a solid arrow.

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Discussion

Polypeptide growth factors elicit biological effects through binding to their cognate cell surface receptors. Receptors can be grouped into several classes based on their structure and mechanism of action. These classifications include the protein tyrosine kinases (PTKs), the serine/threonine kinases, and the cytokine receptors. Receptor PTK signaling is initiated by a direct interaction with ligand, which induces receptor dimerization or oligomerization that in turn leads to receptor autophosphorylation. The activated receptor then recruits and phosphorylates intracellular substrates, initiating a cascade of events which culminates in a biological response (Schlessinger and Ullrich, Neuron 9, 383-391, 1992). In contrast, signal transduction by serine/threonine kinase or cytokine receptors often involves formation of multi-component receptor complexes in which the ligand binding and signal transducing components are distinct. Examples are the TGF-receptor complex, a serine/threonine kinase receptor consisting of separate binding (Type II) and signaling (Type I) components and the CNTF family. CNTF, interleukin-6 (IL-6) and leukocyte inhibitory factor (LIF) share the common

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signaling components, gp130 and/or LIFR, in their respective receptor complexes. While the ligand specificity of these complexes is determined by a specific binding subunit to each individual ligand, signal transduction requires association of the initial complex of ligand and ligand binding subunit with other receptor subunits which cannot bind ligand directly (Ip et al., Cell. 69, 1121-1132, 1992). In the CNTF receptor complex, the ligand binding component is CNTF receptor (CNTFR), which like GDNFR, is a GPI-anchored membrane protein. The present invention involves the description of the first example of a receptor PTK whose autophosphorylation is dependent upon association with a separate ligand-specific binding component.

The present study confirms that GDNFR- α , a GPI-linked membrane protein that binds to GDNF with high affinity, is required for the efficient association of GDNF with the Ret receptor PTK. In the absence of GDNFR- α , GDNF is unable to bind to Ret or stimulate Ret receptor autophosphorylation. In the presence of GDNFR- α , GDNF associates with Ret and rapidly induces Ret autophosphorylation in a dose-dependent manner. GDNFR- α is able to function in either membrane bound or soluble forms (Figure 11), as discussed above. GDNF concentrations of 50 pg/mL (1.7 pM) are able activate the Ret tyrosine kinase in cells expressing GDNFR- α . This is consistent with the dissociation constant (1.5 pM) found for the high affinity GDNF binding sites on NGR-38 cells. The rapid induction of Ret phosphorylation by GDNF (detectable one minute after treatment) and the ability of Ret-Fc to block autophosphorylation suggest that Ret is being activated directly rather than as a downstream consequence of the phosphorylation of some other receptor.

Cross-linking studies support the hypothesis that efficient association of Ret with GDNF depends on GDNFR- α . Cross-linking of GDNF to Ret in NGR-38 cells which express high levels of GDNFR- α is robust, but in parental Neuro-2a cells cross-linked products are barely detectable. Although conclusive identification of all the cross-linked complexes is difficult, the data clearly demonstrates an association of Ret with GDNF that is dependent on the presence of GDNFR- α , and demonstrates that GDNFR- α is included in some of the cross-linked products. The reason for the presence of minor cross-linked species in Neuro-2a cells is not clear. While the expression of GDNFR- α mRNA in Neuro-2a cells could not be detected by Northern blot, it is possible that GDNFR- α is expressed at very low levels in these cells.

The fact that Ret can be activated by GDNF in cultured rat embryonic spinal cord motor neurons further demonstrates the biological relevance of the Ret/GDNF

interaction. These cells are a primary target of GDNF *in vivo*, and have been shown to respond to low doses of GDNF *in vitro* (Henderson et al., 1994). Stimulation of Ret phosphorylation was abolished when the motor neuron cells were pre-treated with PI-PLC (data not shown), suggesting that the activation of Ret by GDNF requires GDNFR- α .

Although binding of ligand to the receptor extracellular domain is the first step in the activation of other known receptor PTKs, the present data has shown that this is not the case for GDNF and Ret. Figure 13 depicts a model for the binding of GDNF to GDNFR- α and Ret, and the consequent activation of the Ret PTK in response to GDNF. The initial event in this process is the binding of disulfide-linked dimeric GDNF to GDNFR- α in either monomeric or dimeric form. Although there is currently no direct evidence for the existence of dimeric GDNFR- α , when 293T cells were transfected with GDNFR- α cDNA, two classes of binding sites appeared. The simplest explanation for this observation is the existence of monomeric and dimeric GDNFR- α , each with its own ligand binding affinity. This is consistent with the finding that GDNF binding affinities are apparently unaffected by the presence of Ret. Since the present experiments do not address the question of whether dimeric GDNFR- α is in equilibrium with its monomer in the absence of GDNF or if dimerization is induced by GDNF binding, these possibilities are presented as alternate pathways. The complex consisting of dimeric GDNFR- α and dimeric GDNF can bind two molecules of Ret, forming the active signaling complex. As for other PTKs, close contact between the intracellular catalytic domains of two Ret molecules is likely to result in receptor autophosphorylation. This notion that Ret functions by this mechanism is supported by the fact that the MEN2A mutation which causes steady state dimerization of Ret results in constitutive activation of the Ret kinase (Santoro et al., 1995).

Motor neurons have been reported to respond to GDNF with an ED₅₀ of as low as 5 fM (Henderson et al., 1994). Although it is difficult to compare binding affinity with the ED₅₀ for a biological response, it is possible that very high affinity GDNF binding sites exist on these cells. Other cells, such as embryonic chick sympathetic neurons, have been reported to bind GDNF with a K_d of 1-5 nM (Trupp et al., Journal Of Cell Biology. 130, 137-148, 1995). It is unlikely that GDNFR- α is involved in a receptor complex for such low affinity sites, but a weak direct interaction between GDNF and Ret may be present.

Expression of c-ret has been observed during embryogenesis in many cell lineages of the developing central and peripheral nervous systems, including cells of

the enteric nervous system (Pachnis, et al., Development, 119, 1005-1017, 1993; Tsuzuki et al., 1995). Outside the nervous system, c-ret expression has been detected in the Wolffian duct, ureteric bud epithelium and collecting ducts of the kidney (Pachnis, et al., supra; Tsuzuki et al., 1995). Ret expression has also been
5 detected in all neuroblastoma cell lines derived from the neural crest (Ikeda et al., 1990) and from surgically resected neuroblastomas (Nagao et al., 1990; Takahashi & Cooper, 1987). GDNF expression has been observed in both CNS and PNS, as well as in non-neuronal tissues during embryonic development. The levels of GDNF expression found in many non-neuronal tissues were higher than in the nervous
10 system (Choi-Lundberg and Bohn, Brain Res. Dev. Brain Res. 85, 80-88, 1995). Although expression of GDNFR- α has not been extensively studied, primary Northern blot analysis detected the presence of high levels of the GDNFR- α mRNA in the liver, brain, and kidney of adult rat and mouse. The similarity of the expression patterns of ret, GDNF, and GDNFR- α in developing nervous system and
15 kidney is consistent with their combined action during development.

Mammalian kidney development has been postulated to result from reciprocal interactions between the metanephron and the developing ureter, a branch developed from the caudal part of the Wolffian duct (Saxen, Organogenesis of the kidney. Development and Cell Biology series, Cambridge University Press,
20 Cambridge, England, 1987). While the expression of Ret has been found at the ureteric bud but not in the surrounding mesenchyme in developing embryos, the expression of GDNF was detected in the undifferentiated but not adult metanephric cap of the kidney. These observations suggest that an interaction between GDNF and Ret is responsible for initiating the development of the ureteric structure.
25 Further support for this hypothesis is provided by targeted disruptions of the GDNF and ret genes, which result in very similar phenotypic defects in kidney (Schuchardt et al., Nature. 367, 380-383, 1994; Sanchez, in press). Another major phenotypic defect observed in both GDNF (-/-) and ret (-/-) knockout animals is a complete loss of the enteric neurons throughout the digestive tract. Hirschsprung's disease, a
30 genetic disorder characterized by the congenital absence of parasympathetic innervation in the lower intestinal tract, has also been linked to "loss-of-function" mutations in ret (Romeo et al., Nature. 367, 377-378, 1994. Edery et al., 1994). A later report (Angrist et al., Hum. Mol. Genet. 4, 821-830, 1995) indicated that, contrary to earlier observations, some Hirschsprung's patients do not carry
35 mutations in ret. It is now envisioned that such patients may carry mutations in GDNF, GDNFR- α or some other critical component of this signaling pathway.

Experimental Procedures

[¹²⁵I]GDNF Binding to Neuro-2a Cells Expressing GDNFR- α

Neuro-2a cells (ATCC #CCL 131) were transfected with an expression
5 plasmid, as described above, using the Calcium Phosphate Transfection System
(GIBCO/BRL) according to the manufacturer's directions. Transfected cells were
selected for expression of the plasmid by growth in 400 μ g/mL G418 antibiotic
(Sigma). G418 resistant clones were expanded and assayed for GDNFR- α
expression by binding to [¹²⁵I]GDNF (Amersham, Inc., custom iodination, catalog
10 #IMQ1057). Cells from each clone were seeded at a density of 3×10^4 cells/cm² in
duplicate wells of 24-well tissue culture plates (Becton Dickinson) pre-coated with
polyornithine. Cells were washed once with ice-cold washing buffer (DMEM
containing 25 mM HEPES, pH 7.5) and were then incubated with 50 pM
[¹²⁵I]GDNF in binding buffer (washing buffer plus 0.2% BSA) at 4°C for four
15 hours either in the presence or absence of 500 nM unlabeled GDNF. Cells were
then washed four times with ice-cold washing buffer, lysed in 1 M NaOH, and the
cell-associated radiolabel quantitated in a 1470 Wizard Automated Gamma Counter
(Wallac Inc.). The amount of GDNFR- α expressed by individual clones was
estimated by the ratio of [¹²⁵I]GDNF bound to cells in the absence and presence of
20 unlabeled GDNF. Three clones were chosen as representatives of high, moderate,
and low level expressors of GDNFR- α for use in binding experiments. The ratios
[¹²⁵I]GDNF bound in the absence and presence of unlabeled GDNF for these clones
were: NGR-38) 16:1, NGR-16) 12.8:1, and NGR-33) 8:1. Equilibrium binding of
[¹²⁵I]GDNF to NGR-38 cells was carried out as described above except that
25 concentrations of labeled GDNF ranged from 0.5 pM to 1 nM. In all assays,
nonspecific binding as estimated by the amount of radiolabel binding to cells in the
presence of 500 nM unlabeled GDNF was subtracted from binding in the absence of
unlabeled GDNF. Binding data was analyzed by Scatchard plot.

30 Chemical Cross-Linking

Neuro-2a or NGR-38 cells were washed once with phosphate-buffered saline
(PBS, pH 7.1), then treated for four hours at 4°C with 1 or 3 nM [¹²⁵I]GDNF in
binding buffer in the presence or absence of 500 nM unlabeled GDNF. Following
binding, cells were washed four times with ice-cold washing buffer and incubated at
35 room temperature for 45 minutes with 1 mM bis suberate (BS³, Pierce) in washing
buffer. The cross-linking reaction was quenched by washing the cells three times
with Tris-buffered saline (TBS, pH 7.5). The cells were then either lysed directly in

SDS-PAGE sample buffer (80 mM Tris HCl [pH 6.8], 10% glycerol, 1% SDS, 0.025% bromophenol blue) or in Triton X-100 lysis buffer (50 mM Hepes, pH 7.5, 1% Triton X-100, 50 mM NaCl, 50 mM NaF, 10 mM sodium pyrophosphate, 1% aprotinin (Sigma, Cat.# A-6279), 1 mM PMSF (Sigma, Cat.# P-7626), 0.5 mM Na₃VO₄ (Fisher Cat.# S454-50). The lysates were clarified by centrifugation, incubated with 5 µg/mL of anti-Ret antibody (Santa Cruz Antibody, C-19, Cat. #SC-167), and the resulting immunocomplexes were collected by precipitation with protein A-Sepharose CL-4B (Pharmacia). The immunoprecipitates were washed three times with the lysis buffer, once with 0.5% NP-40 containing 50 mM NaCl and 20 mM Tris-Cl, pH 7.5, and were then resuspended in SDS-PAGE sample buffer. Both the whole cell lysates and the immunoprecipitates were fractionated by 7.5% SDS-PAGE with a ratio of Bis:Acrylamide at 1:200.

Western Blot Analysis

The autophosphorylation of Ret receptor was examined by Western blot analysis. Briefly, cells were seeded 24 hours prior to the assay in 6-well tissue culture dishes at a density of 1.5×10^6 cells /well. Cells were washed once with binding buffer and treated with various concentrations of different reagents (including GDNF, PI-PLC, PI-PLC/CM, and Ret-Fc fusion protein), either alone or in combination, in binding buffer for various periods of times. Treated cells and untreated controls were lysed in Triton X-100 lysis buffer and immunoprecipitated with the anti-Ret antibody (Santa Cruz, C-19, Cat. #SC-167) and protein-A Sepharose as described above. Immunoprecipitates were fractionated by SDS-PAGE and transferred to nitrocellulose membranes as described by Harlow and Lane (Antibodies: A Laboratory Manual. Cold Spring Harbor Laboratory: Cold Spring Harbor, New York, 1988). The membranes were pre-blocked with 5% BSA (Sigma) and the level of tyrosine phosphorylation of the receptor was determined by blotting the membrane with an anti-phosphotyrosine monoclonal antibody 4G10 (UBI, Cat. #05-321) at room temperature for two hours. The amount of protein included in each lane was determined by stripping and re-probing the same membrane with the anti-Ret antibody. Finally, the membrane was treated with chemiluminescence reagents (ECL, Amersham) following the manufacturer's instructions and exposed to X-ray films (Hyperfilm-ELC, Amersham).

Treatment of Cells with PI-PLC and Generation of PI-PLC Treated Conditioned Media

In order to release GPI-linked GDNFR- α from the cell surface, cells were

washed once with washing buffer, then incubated with 1 U/mL phosphatidylinositol specific phospholipase C (PI-PLC, Boehringer Mannheim, Cat. #1143069) in binding buffer at 37°C for 45 minutes. The cells were then washed three times with washing buffer and further processed for Ret autophosphorylation assay or cross-linking. For generation of PI-PLC treated conditioned media (PI-PLC/CM), 8 x 10⁶ cells were removed from tissue culture dishes by treating the cells with PBS containing 2 mM of EDTA at 37°C for 5 to 10 minutes. Cells were washed once with washing buffer, resuspended in 1 mL of binding buffer containing 1 U/mL of PI-PLC, and incubated at 37°C for 45 minutes. The cells were pelleted, and the PI-PLC/CM was collected.

Preparation of the Ret-Fc Fusion Protein

A cDNA encompassing the entire coding region of c-Ret was isolated from a day 17 rat placenta cDNA library using an oligonucleotide probe corresponding to the first 20 amino acids of the mouse c-Ret (Iwamoto et al., 1993; van Heyningen, 1994). The region coding for the extracellular domain of the Ret receptor (ending with the last amino acid, R636) was fused in-frame with the DNA coding for the Fc region of human IgG (IgG1) and subcloned into the expression vector pDSR2 as previously described (Bartley et al., Nature. 368, 558-560, 1994). The ret-Fc/pDSRa2 plasmid was transfected into Chinese hamster ovary (CHO) cells and the recombinant Ret-Fc fusion protein was purified by affinity chromatography using a Ni⁺⁺ column (Qiagen).

Preparation of Embryonic Rat Spinal Cord Motor Neuron Cultures

Enriched embryonic rat spinal cord motor neuron cultures were prepared from entire spinal cords of E15 Sprague-Dawley rat fetuses 24 hours before the experiments. The spinal cords were dissected, and the meninges and dorsal root ganglia (DRGs) were removed. The spinal cords were cut into smaller fragments and digested with papain in L15 medium (Papain Kit, Worthington). The motor neurons, which are larger than other types of cells included in the dissociated cell suspension, were enriched using a 6.8% Metrizamide gradient (Camu and Henderson, J Neuroscience. 44, 59-70, 1992). Enriched motor neurons residing at the interface between the metrizamide cushion and the cell suspension were collected, washed, and seeded in tissue culture dishes pre-coated with poly-L-ornithine and laminin at a density of ~9 x 10⁴ cells/cm² and were cultured at 37°C.

Example 10

GRR2 Mediation of Neurturin and GDNF-Induced Ret Activation

The present study demonstrates that neurturin binds to both GDNFR- α and
5 GRR2, a novel receptor related to GDNFR- α . Both GDNFR- α and GRR2 can
mediate neurturin-induced autophosphorylation of the Ret protein tyrosine kinase.
GDNF also binds both GDNFR- α and GRR2, and activates Ret in the presence of
either binding receptor. However, neurturin binds GRR2 more effectively than
GDNF, while GDNF binds GDNFR- α more efficiently than neurturin. These data
10 indicate that, while there is crosstalk, GDNF is the primary ligand for GDNFR- α and
neurturin appears to exhibit a preference for GRR2.

Introduction

15 Recently, Kotzbauer et al. (Nature, 384, 467-470, 1996) reported the cloning
of neurturin, a novel neurotrophic factor that is approximately 42% identical in
amino acid sequence to GDNF. Both GDNF and neurturin are synthesized in pre-
pro forms and their precursor molecules are proteolytically processed to yield mature
proteins of about 100 amino acids that assemble into disulfide-linked homodimers.
20 All seven cysteine residues crucial for the structure of GDNF and their spacing
patterns are conserved in neurturin (Kotzbauer et al., 1996). Although the biological
activities of neurturin have not yet been thoroughly investigated, they appear to be
very similar to those of GDNF. Both neurturin and GDNF have been shown to
promote the survival of sympathetic neurons derived from the superior cervical
25 ganglia (SCG) and of sensory neurons of both the nodose (NG) and dorsal root
ganglia (DRG). Neurturin and GDNF mRNAs are widely distributed in a variety of
both neuronal and non-neuronal tissues of embryos and adults. Both are found in
brain, kidney, and lung, whereas neurturin mRNA is also expressed at high levels in
neonatal blood.
30 The structural and biological similarities between GDNF and neurturin
suggest that their action may be mediated by the same or related receptors. The
receptor for GDNF consists of a complex of GDNF receptor α (GDNFR- α) and the
Ret protein tyrosine kinase (PTK) (Jing et al., Cell, 85, 1113-1124, 1996; Treanor et

al., Nature, 382, 80-83, 1996). GDNFR- α is a glycosyl-phosphatidylinositol (GPI) anchored cell surface molecule that serves to bind GDNF but cannot signal independently since it lacks a cytoplasmic domain. GDNF signaling is accomplished via association of the complex of GDNF and GDNFR- α with Ret,
5 resulting in activation of the Ret kinase.

GDNFR- α mRNA is widely distributed in neuronal and nonneuronal tissues and is expressed through embryonic development to adulthood, implying a broad spectrum of biological functions (Treanor et al., 1996; Fox et al., unpublished data). The other component of the GDNF receptor complex, Ret, is a receptor type PTK
10 encoded by the *ret* proto-oncogene. Ret mRNA and protein are highly expressed in the CNS and PNS, as well as in the kidney. Various mutations in the *ret* gene are associated with inherited human diseases, including familial medullary thyroid carcinoma (FMTC), multiple endocrine neoplasia type 2A (MEN2A) and 2B (MEN2B), and Hirschsprung's disease. Targeted disruption of the *ret* gene in
15 knockout mice results in severe phenotypic defects, including renal agenesis or severe dysgenesis and lack of entire enteric nervous system. These defects are extremely similar to those caused by GDNF null mutations, implying that GDNF-mediated signaling through Ret is required for the development of these tissues. Much less severe defects, however, were detected in a number of neuronal structures
20 in which both GDNFR- α and Ret are expressed, such as the trigeminal and vestibular ganglia, the facial motor nucleus, the substantia nigra, and the locus coeruleus (Schuchardt et al., Nature, 367, 380-383, 1994; Treanor et al., 1996). This suggests that either GDNF signaling is not required for the embryonic development of these structures, or that some unknown signaling molecules similar to GDNF or Ret may
25 exist that can substitute for them. Alternatively, the embryonic development of these tissues may completely rely on another yet unknown signaling system.

This example describes the cloning of a novel GDNFR- α related receptor, GRR2, and provides evidence that GRR2 is a receptor for neurturin. Analogous to GDNF and GDNFR- α , neurturin effectively binds GRR2 and induces Ret activation.
30 The data also show that both GDNF and neurturin can interact with either GDNFR- α or GRR2 and activate the Ret PTK in the presence of either binding receptor.

Results

Cloning and Sequence Analysis of GRR2

A human expressed sequence tag (EST) with significant homology to GDNFR- α was found by a FASTA search of the publicly available nucleic acid sequence databases (Marra et al., 1996, WashU-HHMI Mouse EST Project, unpublished). Oligonucleotides corresponding to the ends of this EST were synthesized and used in a reverse transcription-polymerase chain reaction (RT-PCR) with human fetal brain mRNA as the template. A fragment of the expected length was isolated and used as a hybridization probe to screen a human fetal brain cDNA library. Five positive clones were identified and the longest clone was sequenced. This clone contained a large open reading frame coding for a 464 amino acid protein related in sequence to GDNFR- α . We have named this protein GDNFR- α Related Receptor 2 (GRR2). The oligonucleotides described above were also used to screen pools from a rat photoreceptor cDNA library (Jing et al., 1996) by PCR and a product of the expected length was obtained from a single pool. An individual cDNA clone from this pool was identified by hybridization to the radiolabeled PCR product and sequenced. This clone contained a 2.2 kb insert with an open reading coding for a 460 amino acid peptide that is nearly identical to human GRR2.

A comparison of the amino acid sequences of human and rat GDNFR- α and GRR2 is shown in Figure 20. Shaded areas indicate amino acid sequence conservation between all four receptors while boxes indicate conservation only between the same receptor from different species. The amino acid sequences of both GDNFR- α and GRR2 are extremely well-conserved between species, each human receptor being 92% identical to its rat counterpart. The overall amino acid sequence identity between human GDNFR- α (hGDNFR- α) and human GRR2 (hGRR2) is 48%. The sequence is most divergent in the C-terminal region--amino acids 350-465 of hGDNFR- α are only 22% identical to amino acids 361-464 of hGRR2. In the N-terminal region, hGDNFR- α and hGRR2 are more closely related, sharing 56% amino acid identity. The corresponding identities between the rat GDNFR- α and GRR2 (rGDNFR- α and rGRR2) are very similar: 48% overall, 26% in the C-terminal region, and 55% in the N-terminal region. The sequence comparison indicates that GDNFR- α and GRR2 are likely to be structurally very similar. The positions of 30 of the 31 cysteine residues (shown in boldface, Figure

20) found in GDNFR- α are conserved in both human and rat GRR2 (one additional cysteine residue is present near the N-terminus of hGRR2). In addition, the hydrophobic C-terminus involved in GPI-linkage of GDNFR- α to the cell membrane (Jing et al., 1996; Treanor et al., 1996) is also present in GRR2.

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Figure 20. Comparison of GDNFR- α And GRR2 Peptide Sequences

The amino acid sequences of human and rat GDNFR- α and GRR2 are aligned. Shaded areas indicate amino acids that are identical in all four sequences. Boxes indicate conservation between rat and human orthologs of the same receptor, but not between GDNFR- α and GRR2.

10

Both Neurturin And GDNF Bind to LA-N-5 And NGR-38 Cells

LA-N-5 is a human neuroblastoma cell line (Sonnenfeld and Ishii, J. Neuroscience Research, 8:375-391, 1982) that expresses high levels of *ret* mRNA (Bunone et al., Exp. Cell. Res., 217:92-99, 1995). RT-PCR experiments using primers specific to GDNFR- α and GRR2 showed that these cells express GRR2 mRNA, but GDNFR- α mRNA was not detected (data not shown). NGR-38 is a cell line derived from mouse Neuro-2a cells (Jing et al., 1996). It expresses high levels of both GDNFR- α and Ret (Jing et al., 1996), but no detectable GRR2 (data not shown), and binds GDNF specifically. LA-N-5 and NGR-38 cells were incubated with [125 I]-labeled recombinant human neurturin (NTN) or GDNF in the absence or presence of excess unlabeled ligand. As shown in Figure 21A, [125 I]NTN bound to LA-N-5 cells more strongly than [125 I]GDNF, although both bound at detectable levels. The binding of [125 I]NTN to LA-N-5 cells was significantly inhibited by unlabeled neurturin, but not by GDNF. [125 I]GDNF also bound to LA-N-5 cells, however, the binding was inhibited by either cold GDNF or neurturin.

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Figure 21B depicts the binding of [125 I]NTN and [125 I]GDNF to the GDNFR- α expressing cell line NGR-38. Although both [125 I]NTN and [125 I]GDNF bound to NGR-38 cells, [125 I]GDNF bound more strongly. As was observed for LA-N-5 cells, the binding of [125 I]GDNF to NGR-38 cells was inhibited by both unlabeled neurturin and GDNF, while binding of [125 I]NTN was only replaceable by neurturin (Figure 21B).

30

Figure 21. Binding of Neurturin and GDNF to LA-N-5 and NGR-38 Cells

LA-N-5 (A) and NGR-38 (B) cells were incubated with 50 pM of either [¹²⁵I]NTN or [¹²⁵I]GDNF in the absence (light gray bars) or presence of unlabeled GDNF (dark gray bars) or neurturin (black bars) at 4°C for 2 hours. The unbound
5 ligands were removed at the end of the incubation and the radioactivity associated with the cells was determined as described.

Cross-Linking of Neurturin and GDNF to GDNFR-α and GRR2

The binding experiments suggest that both neurturin and GDNF interact with
10 GDNFR-α and GRR2. However, lack of a GRR2 specific antibody made further study of these interactions difficult. To overcome this difficulty, plasmids were generated that transiently express GDNFR-α/Fc and GRR2/Fc fusion proteins when transfected into 293T cells. Conditioned medium (CM) containing either GDNFR-α/Fc or GRR2/Fc fusion proteins was incubated with [¹²⁵I]NTN or [¹²⁵I]GDNF,
15 chemically cross-linked, and then precipitated directly using Protein-A Sepharose beads. The immunoprecipitates were analyzed by SDS-PAGE (Figure 22). Major species of 100-120 kD and 90-110 kD were observed when [¹²⁵I]GDNF or [¹²⁵I]NTN were used, respectively (Figure 22). Strong bands with higher molecular mass, ~300 kD for GDNFR-α/Fc and ~280 kD for GRR2/Fc, were also observed
20 (Figure 22). In addition, minor bands of ~15 kD, 35 kD, and 60 kD in the [¹²⁵I]GDNF lanes and ~12 kD, 26 kD, and 50 kD in the [¹²⁵I]NTN lanes, were visible (Figure 22). When CM from mock transfected cells were used, no cross-linked band was precipitated by Protein-A Sepharose (data not shown). None or much weaker radio-labeled bands were detected when excess unlabeled ligands were
25 added in the control samples (Figure 22).

Figure 22. Chemical Cross-Linking of Neurturin And GDNF to GDNFR-α and GRR2 Receptors.

CM containing GDNFR-α/Fc (GDNFR-α) or GRR2/Fc (GRR2) fusion
30 proteins were incubated with either 10 nM of [¹²⁵I]NTN (N) or 5 nM of [¹²⁵I]GDNF (G) in the presence (+ unlabeled) or absence (- unlabeled) neurturin (N) or GDNF (G). The bound receptor-ligand complexes were chemically cross-linked by 1 mM

of BS³, precipitated with Protein-A Sepharose and analyzed by SDS-PAGE as described. The solid arrow indicates the 90-110 kD and the 100-120 kD cross-linked species. The open arrow depicts the ~280 kD and ~300 kD complexes.

5 Neurturin Induces Ret Autophosphorylation in Cells That Express GDNFR- α

The ability of neurturin to associate with GDNFR- α indicates that neurturin, like GDNF, may activate Ret through GDNFR- α . In order to examine this possibility, the ability of neurturin to induce Ret autophosphorylation in NGR-38 cells was tested. NGR-38 cells were treated with concentrations of neurturin ranging from 0 to 50 nM, lysed, and the lysates immunoprecipitated with anti-Ret antibody. The immunoprecipitates were analyzed by SDS-PAGE followed by immunoblotting using an anti-phosphotyrosine antibody. A 170 kD band, indicating autophosphorylation of tyrosine residues on the mature form of Ret, was observed in all lanes (Figure 23, lanes 8-14 from left). A much weaker corresponding band was observed in neurturin-treated Neuro-2a cells (data not shown). The induction of Ret autophosphorylation by neurturin was dose-dependent. Stimulation of Ret autophosphorylation in NGR-38 cells could be detected with 500 pM neurturin (Figure 23). In a parallel experiment using GDNF in place of neurturin, an increase in the level of phosphorylation of the 170 kD Ret band over background could be seen at a GDNF concentration of 5 pM (Figure 23, lanes 1-7 from left). When the filters were stripped and re-probed with the anti-Ret antibody, the 170 kD Ret protein band appeared in all lanes with approximately equal intensity (data not shown).

25 Figure 23. Neurturin and GDNF Induce Ret Autophosphorylation in NGR-38 Cells

NGR-38 cells were treated with various concentrations of GDNF or neurturin as described. The cells were lysed, immunoprecipitated with anti-Ret antibody, fractionated by SDS-PAGE, and blotted with anti-phosphotyrosine antibody for Ret phosphorylation. The bands of phosphorylated Ret are indicated by an arrow.

30

Neurturin And GDNF Induce Ret Autophosphorylation in LA-N-5 Cells

Both neurturin and GDNF bind to GRR2, and the Ret PTK can be activated by either neurturin or GDNF through GDNFR- α . These observations suggest that

GRR2 may also be able to mediate neurturin and/or GDNF activation of Ret. To assess this possibility, human LA-N-5 neuroblastoma cells expressing GRR2 and Ret were treated with various concentrations of neurturin or GDNF and processed for immunoblotting as described in the previous section (Figure 24). As shown, both
5 neurturin and GDNF induced Ret autophosphorylation (Figure 24).

Figure 24. Neurturin And GDNF Induced Ret Autophosphorylation in LA-N-5 Cells

LA-N-5 cells were treated with various concentrations of GDNF or neurturin as described. The cells were lysed, immunoprecipitated with anti-Ret antibody,
10 fractionated by SDS-PAGE, and blotted with anti-phosphotyrosine antibody for Ret phosphorylation. The bands of phosphorylated Ret are indicated by an arrow.

Neurturin And GDNF Induce MAP Kinase activation in LA-N-5 And NGR-38 Cells

We have demonstrated that both neurturin and GDNF can induce Ret
15 autophosphorylation in cells expressing either GDNFR- α or GRR2. We then tested if the activation of Ret kinase by neurturin and/or GDNF could lead to activation of the downstream signaling molecule MAP kinase. Both LA-N-5 and NGR-38 cells were treated with either neurturin, GDNF, or NGF. Treated cells were lysed directly in SDS-PAGE sample buffer, fractionated by SDS-PAGE, and immunoblotted using
20 an anti-phosphorylated MAP kinase antibody (New England Biolabs, Beverly, MA). As shown in Figure 25, both p44 and p42 isoforms of MAP kinase are apparently activated by both neurturin and GDNF in either LA-N-5 or NGR-38 cells. MAP kinase activation by NGF (used as a positive control) was also observed.

25 Figure 25 (Panels A and B). Neurturin And GDNF Induced MAP Kinase Activation in LA-N-5 And NGR-38 Cells

25A. LA-N-5 cells were treated with various concentrations of GDNF or neurturin as described. The cells were lysed directly in 2 X SDS-PAGE sample buffer containing 0.5 mM NaVO₄, fractionated by SDS-PAGE, and blotted with an
30 antibody against phosphorylated MAP kinase (MAPK-P). 25B. The membrane was stripped and reprobed with an anti-MAP kinase antibody for the amount of MAP kinase proteins loaded in each lane (MAPK).

Discussion

Signal transduction by most receptor PTKs starts by direct interaction with their ligands and consequent activation of the receptors. Cloning and
5 characterization of GDNFR- α , an accessory molecule for ligand binding, revealed a novel mechanism by which Ret receptor PTK transduces the GDNF signal. GDNF does not bind Ret alone, instead, it first binds to GDNFR- α and then interacts with Ret as a part of the GDNF-GDNFR- α complex. The newly cloned GRR2 is related to GDNFR- α at both the amino acid level and the three dimensional structure. It
10 shares 48% identical amino acid residues with GDNFR- α , among which are 30 of the 31 cysteines.

We have demonstrated that both neurturin and GDNF bind to GDNFR- α and GRR2. Binding of GDNF or neurturin to either GDNFR- α or GRR2 results in further association of the ligand with Ret and consequent activation of the Ret PTK
15 and the MAP kinase, a downstream signaling molecule. However, each of the ligands appears to bind to one receptor preferentially. Neurturin binds GRR2 expressing LA-N-5 cells more efficiently than GDNF, and GDNF binds GDNFR- α expressing NGR-38 cells more efficiently than neurturin. It is not clear at this time why the binding of [¹²⁵I]GDNF to both GDNFR- α and GRR2 can be replaced by
20 both unlabeled GDNF and neurturin, but that of [¹²⁵I]NTN can only be inhibited by cold neurturin.

Consistent with the binding study, GDNF is more effectively cross-linked to GDNFR- α /Fc fusion receptors than to GRR2/Fc, while neurturin cross-linking shows the opposite result.

25

Experimental Procedures

cDNA Cloning of GRR2

A search of the GenBank database for sequences related to GDNFR- α
30 resulted in the identification of EST, H12981.Gb_Est1. Primers corresponding to nucleotides 47 to 65 (5'-CTGCAAGAAGCTGCGCTCC-3') and 244 to 265 (5'-CTTGTCTCATAGGAGCAGC-3') of H12981.Gb_Est1 were synthesized and used for RT-PCR with human fetal brain mRNA (Clontech, Cat. #64019-1) as the

template. A 218 nt fragment was amplified, subcloned into pBlue-Script (Stratagene, La Jolla, CA), and sequenced to verify its correspondence with the original EST. The fragment was then radiolabeled with [³²P]-dCTP using a Random Primed DNA Labeling Kit (Stratagene, La Jolla, CA) according to the
5 manufacturer's instructions. The radio-labeled probe was used to screen a human fetal brain cDNA library (Stratagene, La Jolla, CA). Two million clones were plated on 15 cm agarose plates and replicated on duplicate nitrocellulose filters. The filters were prehybridized at 55°C for 3.5 hours in 200 ml of 6 x SSC, 1 x Denhardt's, 0.5% SDS, and 50 µg/ml salmon sperm DNA. Following the addition of 2 x 10⁸ cpm of
10 the radiolabeled probe, hybridization was continued for 18 hours. Filters were then washed twice for 30 minutes each at 55°C in 0.2 x SSC, 0.1% SDS and exposed to X-ray film overnight with an intensifying screen. Five positive clones were identified and their DNA sequences were determined.

15 The oligonucleotide primers described above were also used for PCR screening of DNAs isolated from 27 pools (1500 clones each) of a rat photoreceptor cDNA library (Jing et al., 1996). A single positive pool was identified and screened by hybridization to the same radio-labeled probe as described above. An individual cDNA clone from this pool was identified and sequenced.

20

DNA Sequencing and Sequence Analysis

DNA sequencing was performed using an automated Applied Biosystems 373A DNA sequencer and Taq DyeDeoxy Terminator cycle sequencing kits (Applied Biosystems, Foster City CA). Comparison of the GDNFR-α and GRR2
25 sequences with public databases was carried out using the FASTA computer algorithm (Pearson and Lipman, Proceedings Of The National Academy Of Sciences Of The United States Of America. 85, 2444-2448, 1988). The peptide sequences of GDNFR-α and GRR2 were aligned using the Lineup program. All sequence analysis programs used were included in the Wisconsin sequence analysis package
30 (Wisconsin Package Version 9.0, Genetics Computer Group, Madison, WI).

Binding of [¹²⁵I]GDNF and [¹²⁵I]JNTN to NGR-38 and LA-N-5 Cells

Recombinant human neurturin was expressed in *E. coli* as insoluble protein. The inclusion bodies were solubilized, and the neurturin protein was re-folded and purified by ion exchange and hydrophobic interaction chromatography.

[¹²⁵I]NTN (~2000 Ci/mmol) was prepared using purified *E. coli* expressed protein (Amersham, Inc., Arlington Heights, IL; custom iodination, catalog #IMQ1057). Recombinant human GDNF was also radio-iodinated (Jing et al., 1996). Binding of [¹²⁵I]NTN and [¹²⁵I]GDNF to LA-N-5 and NGR-38 cells were carried out as previously described (Jing et al., 1990). Briefly, cells were seeded one day before the assay in 24-well Costar tissue culture plates pre-coated with polyornithine at a density of 3×10^4 cells/cm². Cells were placed on ice for 5 to 10 minutes, washed once with ice-cold buffer (DMEM containing 25 mM HEPES [pH 7.0]) and incubated at 4°C in 0.2 ml binding buffer (washing buffer containing 2 mg/ml bovine serum albumin) containing various concentrations of [¹²⁵I]NTN or [¹²⁵I]GDNF in the absence or presence of 500 nM unlabeled ligands for 4 hours. Cells were washed 4 times with 0.5 ml ice-cold washing buffer and lysed with 0.5 ml of 1 M NaOH. The lysates were counted in a 1470 Wizard Automatic Gamma Counter (Wallac Inc., Gaithersburg, MD).

Chemical Cross-Linking

The coding regions of the first 455 amino acids of human GDNFR- α and the first 451 residues of human GRR2 cDNAs were fused in frame with a DNA fragment encoding the Fc region of human IgG1 tagged with 6 histidine residues at the carboxy terminus (Culouscou et al., J. Biochem., 270:12857-12863, 1995). This construct was then inserted into the expression vector pBK RSV (Stratagene, La Jolla, CA) as previously described (Jing et al., 1996). The GDNFR- α /Fc and GRR2/Fc fusion constructs were transfected into 293T cells, and conditioned media (CM, DMEM supplied with 0.5% fetal calf serum) containing the fusion proteins were collected 4 days after transfection. Aliquots of 1 ml CM plus 50 μ l of 1 M HEPES, pH 7.5 were incubated at 4°C with 10 nM of [¹²⁵I]NTN or 5 nM [¹²⁵I]GDNF in the presence or absence of 1 μ M of unlabeled ligand for 4 hours. Bis suberate (BS³ Pierce, Rockford, IL) stock solution in washing buffer (40 mM) was added to each binding mixture to a final concentration of 1 mM, mixed and

- incubated at room temperature for 30 minutes. The reaction was quenched by adding 50 μ l of 1 M glycine and incubating at room temperature for 15 minutes. Triton X-100 was added to a final concentration of 1%, and the cross-linked product was precipitated directly with 200 μ l of Protein-A Sepharose CL-4B (Pharmacia).
- 5 The cross-linked products were analyzed by 7.5% SDS-PAGE under reducing conditions.

Immunoblotting Analysis

- Ret autophosphorylation was examined by immunoblot analysis as previously described (Jing et al., 1996). Briefly, cells were seeded 24 hours prior to the assay in 6-well tissue culture dishes at a density of 1.5×10^6 cells /well. Cells were washed once with binding buffer and treated with various concentrations of neurturin or GDNF (0.5 pM - 50 nM) in binding buffer at 37°C for 10 minutes. Treated cells and untreated controls were lysed in Triton X-100 lysis buffer (50 mM
- 15 HEPES, pH 7.5, 1% Triton X-100, 50 mM NaCl, 50 mM NaF, 10 mM sodium pyrophosphate, 1% aprotinin (Sigma, Cat.# A-6279), 1 mM PMSF (Sigma, Cat.# P-7626), 0.5 mM Na_3VO_4 (Fisher Cat.# S454-50) and immunoprecipitated with an anti-Ret antibody (Santa Cruz Biotechnology) and protein-A Sepharose as described (Jing et al., 1996). Immunoprecipitates were fractionated by 7.5% SDS-PAGE and
- 20 transferred to nitrocellulose membranes as described by Harlow and Lane (Antibodies Laboratory Manual, Spring Harbor Laboratory, Spring Harbor Press, 1988). The membranes were blocked with 5% BSA (Sigma) and tyrosine phosphorylation of the Ret receptor was detected by probing with an anti-phosphotyrosine monoclonal antibody 4G10 (UBI, Cat #05-321) at room
- 25 temperature for 2 hours. The amount of Ret protein in each lane was determined by stripping and re-probing the same membrane with the anti-Ret antibody. Detection was accomplished using a sheep anti-mouse secondary antibody or protein-A conjugated to horseradish peroxidase (Amersham, cat.#NA931) in conjunction with chemiluminescence reagents (ECL, Amersham) following the manufacturer's
- 30 instructions.

Activation of the MAP kinases was analyzed using a PhosphoPlus MAPK Antibody Kit (New England Biolabs, Beverly, MA, Cat. #9100) following manufacturer's instructions. LA-N-5 and NGR-38 cells were seeded in 6-well dishes

as described above. Cells were quiesced in DMEM containing 0.5% fetal calf serum (FCS) at 37°C for 24 hours. The cells were then incubated with fresh media for 2 hours, treated with 50 ng/ml of NGF, GDNF, or neurturin at 37°C for 5 minutes, and lysed directly in 150 µl of 2 X SDS-PAGE sample buffer containing 0.5 mM NaVO₄. The cell lysates were fractionated by 10% SDS-PAGE and transferred to a nitrocellulose filter. The filter was blocked with 5% non-fat dry milk at 4°C overnight and then incubated overnight at 4°C with a 1:1000 dilution of anti-phosphorylated MAP kinase antibody in the same buffer (New England Biolabs). Bands were detected using a horseradish peroxidase conjugated anti-rabbit antibody and the LumiGLO chemiluminescent reagents according to the manufacturer's recommendations. After exposure to X-ray film, the filter was stripped and reprobed by the anti-MAPK antibody.

Figure 25 (Panels A and B). Neurturin And GDNF Induced MAP Kinase Activation in LA-N-5 And NGR-38 Cells

25A. LA-N-5 cells were treated with various concentrations of GDNF or neurturin as described. The cells were lysed directly in 2 X SDS-PAGE sample buffer containing 0.5 mM NaVO₄, fractionated by SDS-PAGE, and blotted with an antibody against phosphorylated MAP kinase (MAPK-P). 25B. The membrane was stripped and reprobed with an anti-MAP kinase antibody for the amount of MAP kinase proteins loaded in each lane (MAPK).

Example 11

Cloning and Expression of GRR2 and GRR3

Signaling by glial cell line-derived neurotrophic factor (GDNF) is mediated by two receptor components. GDNF receptor- α (GDNFR- α) binds GDNF specifically, leading to the association of GDNF with Ret and the activation of the Ret kinase. Similarly, neurturin induces Ret activation through association with GRR2, a GDNFR- α -related receptor. Both GDNFR- α and GRR2 are capable of binding either GDNF or neurturin, but each exhibits a marked preference for its cognate ligand. A third molecule was cloned and is related in structure and primary

amino acid sequence to GDNFR- α and GRR2. This molecule has been named GDNFR- α -related receptor 3 (GRR3). Analysis of the tissue distribution of GDNFR- α , GRR2, GRR3, and Ret by mRNA blot and *in situ* hybridization reveals overlapping but distinct patterns of expression. Consistent with their role in GDNF function, GDNFR- α and *ret* are co-expressed at known sites of GDNF action. GRR2 and GRR3 transcripts are also co-localized with those of *ret* in some cases, suggesting that GRR3 may also mediate Ret activation by GDNF or a related ligand.

Introduction

10

Glial cell line-derived neurotrophic factor (GDNF) is a potent survival factor for midbrain dopaminergic neurons, motor neurons, and several other types of neuronal cells. Targeted disruption of the GDNF gene in mice causes complete renal agenesis and the absence of enteric neurons (Moore et al., Nature, 382, 76-79, 1996; Pichel et al., Nature, 382, 73-76, 1996; Sanchez et al., Nature, 382, 70-73, 1996; and Hudson et al., Brain Research Bulletin, 36, 425-32, 1995), indicating an essential role for GDNF in the development of the renal and the enteric nervous systems. The GDNF receptor was discovered to consist of a novel ligand binding component, GDNFR- α , and a signaling component, the Ret receptor protein tyrosine kinase.

20

GDNFR- α is attached to the cell membrane through a glycosyl-phosphatidylinositol (GPI) linkage but has no cytoplasmic domain. It binds GDNF specifically and with high affinity regardless of whether or not Ret is present. Ret is a receptor protein tyrosine kinase (PTK) originally discovered as a large open reading frame in the *ret* proto-oncogene. Its unique extracellular domain structure, which includes a signal peptide, a cadherin-like motif, and a cysteine-rich region, places it outside any other known receptor PTK sub-family. Ret alone does not bind GDNF, but was found to form a complex with GDNF and GDNFR- α that results in Ret activation. Activation of the Ret kinase appears to be associated with the biological effects of GDNF. Targeted disruption of the Ret PTK gene results in a phenotype nearly identical to that resulting from the disruption of GDNF (Schuchardt et al., Nature, 367, 380-383, 1994). *In situ* hybridization and immunohistochemical analysis detects high level expression of *ret* mRNA and protein in the developing central and peripheral nervous systems and in the excretory

30

system of the mouse embryo. This expression pattern is similar to that of GDNF and is consistent with Ret's role in GDNF signaling.

The expression pattern of GDNFR- α is also consistent with its involvement in GDNF signaling. GDNFR- α mRNA has been found in a number of GDNF-responsive cell types and structures of the nervous system, often colocalized with *ret*. In the central nervous system, GDNFR- α mRNA has been observed in both developing and adult rat ventral midbrain, facial nucleus and ventral spinal cord. In addition, some specific cells in the superior colliculus, the lateral septum, the molecular layer of cerebellum adjacent to Purkinje cells, and some nuclei in cerebral cortex and the dorsomedial tegmental area have been shown to express GDNFR- α . In the peripheral nervous system, GDNFR- α mRNA expression has been found in subpopulations of neurons in dorsal root ganglia, in enteric neurons, and in neurons from sympathetic ganglia. High levels of GDNFR- α mRNA expression were also observed in other regions of the nervous system, including the retina, thalamus, pons, and medulla oblongata. Expression has also been seen in non-neuronal tissues such as the developing nephrons, pituitary, urogenital tract and pancreatic primordium.

Neurturin is a molecule which has similarities to GDNF in both amino acid sequence and biological activity. The GRR2 protein (GDNFR- α -Related Receptor 2), is a novel protein related in amino acid sequence to GDNFR- α . GRR2 is capable of binding both GDNF and neurturin, and like GDNFR- α , mediates the activation of the Ret PTK in response to these ligands. Although both GDNF and neurturin can bind both GDNFR- α and GRR2, GDNF exhibits a marked preference for GDNFR- α while neurturin interacts more strongly with GRR2. GDNFR- α -Related Receptor 3 (GRR3) a third member of this receptor family has also been found. The present study examines the tissue and cell-specific mRNA expression of GDNFR- α , GRR2, GRR3, and *ret*.

Results

Molecular Cloning and Sequence Comparison of GRR3 with GRR2 and GDNFR- α

Examination of publicly available sequence databases revealed the presence of a short expressed sequence tag (EST) with sequence homology to the GDNFR- α and GRR2 cDNA clones (WashU-HHMI Mouse EST Project). Oligonucleotides

corresponding to the ends of this EST were used as primers in a reverse transcription-polymerase chain reaction (RT-PCR) with total rat embryo RNA as the template. A 225 nucleotide (nt) fragment was amplified, cloned into a plasmid vector, and sequenced to verify that it corresponded to the original GDNFR- α /GRR2-related EST. Plasmid DNAs isolated from pools of an E15 rat embryo cDNA library were screened by PCR and a single positive pool was found. Clones from this pool were screened by hybridization to the radiolabeled 225 nt PCR fragment and a single positive clone was isolated. Sequence analysis of the 1.8 kb insert from this clone revealed an open reading frame coding for a 397 amino acid peptide related to both GDNFR- α and GRR2. This protein was designated GDNFR- α -related receptor 3 (GRR3).

An alignment of the amino acid sequences of rat GDNFR- α , GRR2, and GRR3 is shown in Figure 26. The overall amino acid sequence identity among the three receptors is in the range of 30%-50%. GDNFR- α and GRR2 are somewhat more closely related to each other (48% identity) than they are to GRR3 (35% and 33% identity, respectively). Hydrophobic regions are found at both the amino and carboxy termini of all three molecules, except for the amino terminus of GRR2 (underlined, Figure 26). The amino terminal regions of both GDNFR- α and GRR3 have the characteristics expected for signal peptide sequences. Although the GRR2 N-terminal sequence does not fit the criteria for a classical signal peptide, there is evidence that GRR2 is secreted. The carboxy terminal hydrophobic region of GDNFR- α is known to be involved in GPI-linkage to the cell membrane, and it is likely that the corresponding regions in GRR2 and GRR3 serve the same purpose. The most striking feature of the sequence alignment is the conservation of 28 cysteine residues among all three receptors (highlighted, Figure 26), indicating that these proteins probably have similar three-dimensional structures. Several potential N-glycosylation sites are present in the receptors (shown in boldface, Figure 26), but none are found at the same position in all three receptors. GDNFR- α and GRR2 share sites at positions 365 and 427 that are not found in GRR3, and GRR2 shares a possible site with GRR3 at positions 322-323 (Figure 26).

Expression of GDNFR- α , GRR2, and GRR3 in Adult Rat

The expression of GDNFR- α , GRR2 and GRR3 mRNAs in adult rat tissues was examined by blot hybridization analysis. GDNFR- α mRNA is widely expressed, with high levels found in lung, brain, liver, kidney and spleen.

- 5 Expression is also detectable in heart and among the tissues examined is absent only in muscle and testis. Two distinct size transcripts are observed and their relative amounts vary among the tissues. The 3.6 kb transcript is predominant in liver, lung, heart, and spleen while comparable amounts of the 3.6 kb and 8.5 kb transcripts are present in brain and kidney. The tissue distribution of GRR2 mRNA is similar to
10 that of GDNFR- α . GRR2 expression is highest in lung, spleen and brain, with lesser amounts in kidney and heart. One difference is the lack of GRR2 expression in liver. The size of the GRR2 transcripts is approximately 3.6 kb, similar to the smaller of the two GDNFR- α transcripts. The expression of GRR3 mRNA is highest in kidney and is absent in brain. Detectable expression of GRR3 is also present in spleen,
15 lung, liver, and heart. The transcript size for GRR3 is somewhat smaller (~2.1 kb) than that observed for GDNFR- α and GRR2.

Expression of GDNFR- α , GRR2 and GRR3 in Mouse Embryo

- Developmental expression of GDNFR- α , GRR2, and GRR3 mRNA was
20 examined in the mouse on embryonic days 7, 11, 15, and 17. Expression of the 3.6 kb transcript of GDNFR- α is first apparent at E11, seems to decrease somewhat at E15, but then increases dramatically by E17. A minor amount of the 8.5 kb GDNFR- α mRNA can be detected on E11, but no expression of this transcript is detected thereafter. The expression of the 3.6 kb GRR2 transcript is barely
25 detectable at E11, but increases gradually through E17. Expression of the 2.1 kb GRR3 mRNA is not detected at E7, but is quite strong by E11. After E11, expression decreases and remains constant from E15-E17.

In situ Hybridization Analysis of the Expression of GDNFR- α , GRR2, and GRR3

- 30 In order to provide clues to the potential roles and functional sites of GDNFR- α , GRR2 and GRR3, their expression was examined in regions where biological effects of GDNF have been demonstrated. In the E18 rat embryo, GDNF is highly expressed in the growing ureteric buds and maturing nephrons of the

kidney as well as in the enteric neurons of the intestine. GDNFR- α is found in the same regions of the kidney and intestine as GDNF, but is also expressed at moderate levels in both the dorsal and ventral spinal cord. *ret* is expressed in the kidney and intestine as well, although its expression in the kidney seems to be confined to the ureteric buds. Expression of *ret* is high in the ventral motor neurons, but low in the dorsal region of the spinal cord. Like *ret*, expression of GRR2 in the kidney is restricted to the ureteric buds. GRR2 is expressed in both the dorsal and ventral regions of the spinal cord. A weak, diffuse hybridization signal was detected in the liver for GDNF, *ret*, and GDNFR- α .

10 In the postnatal day 7 rat, *ret* expression can be detected at substantial levels in the substantia nigra, trigeminal ganglia, and at a lower level in the reticular thalamic nucleus. GDNFR- α expression is high in both the reticular and ventromedial thalamic nuclei as well as in the medial habenular nucleus. Moderate expression of GDNFR- α is observed in the substantia nigra and lower but detectable levels are found in the hippocampus. GRR2 is expressed at moderate levels in the reticular thalamic nucleus, ventromedial thalamic nucleus, cerebral cortex (especially the cingulate cortex), and the substantia nigra. We could detect no expression of GRR3 in the P7 rat brain, but significant expression could be detected in the trigeminal ganglia.

20

Discussion

This study describes the isolation of GRR3, a novel molecule related to GDNFR- α and GRR2 and compares the tissue expression of *ret* with that of all three members of the GDNFR receptor family. GRR2 is 48% identical in amino acid sequence to GDNFR- α , while GRR3 is somewhat more distantly related at 35% identity. The position of 28 cysteine residues are conserved in all three molecules. Like GDNFR- α , both GRR2 and GRR3 have hydrophobic C-termini that are likely to be involved in GPI linkage to the cell membrane, and neither has a cytoplasmic domain. This strong conservation of sequence and structural features suggests that GDNFR- α , GRR2, and GRR3 define a new family of receptors for GDNF and related ligands. GDNF signaling is initiated by binding to GDNFR- α and accomplished by association and consequent activation of the Ret PTK. Based upon

its sequence and structural similarities to GDNFR- α and GRR2, GRR3 is likely to function as a binding partner for GDNF, neurturin, and/or some other as yet undiscovered member of this ligand family.

The expression patterns of GDNFR- α , GRR2, and GRR3 in adult rat tissues are similar but distinct. All three mRNAs are found in lung, spleen, heart, and kidney while none of the three show significant expression in muscle or testis. Adult brain exhibits high expression of GDNFR- α and GRR2 mRNAs, but little or no GRR3 is detected. Expression of GDNFR- α mRNA is high in liver while GRR2 mRNA is almost nonexistent. If GDNF, neurturin and other as yet undiscovered GDNF-like ligands signal exclusively through Ret, differences in expression patterns of the ligand-specific binding receptors could provide a mechanism for ligand tissue specificity. Since the expression of *c-ret* can be detected throughout the period from E8.5 to E16.5, differences in the temporal expression of the receptor proteins could also define ligand specificity during development.

Expression of all the receptors and of *c-ret* is high in the adult kidney, the site of the most severe defects found in Ret knockout animals. *In situ* hybridization analyses indicate that *ret*, GDNFR- α , GRR2 and GRR3 are colocalized in several tissues, suggesting that GRR2 and GRR3 may also exert their *in vivo* effects through interaction with Ret (Table 5).

20

Table 5
Expression of *ret*, GDNFR- α , GRR2, and GRR3
in embryonic day 18 rat

	<u><i>ret</i></u>	<u>GDNFR-α</u>	<u>GRR2</u>	<u>GRR3</u>
Kidney/Intestine	+++	+++	++	-*
Brain:				
Thalamic Nuclei:				
Reticular	++	+++	++	-
Ventral medial	+	+++	++	-

Substantia Nigra	+++	+++	+++	-
Habenular nucleus	-	+++	-	-
Hippocampus	+/-	++	-	-
Spinal cord:				
Dorsal	+	++	++	-
Ventral	++	+++	++	-
Trigeminal Ganglia	+++	+++	-	+++

* High levels of expression were detected in the adult kidney.

Both GDNFR- α and GRR2 are transcribed along with *ret* in the kidney and intestine, in the substantia nigra, in the thalamus, and in ventral spinal motor neurons. This finding is consistent with GDNF's ability to promote the survival of dopaminergic and motor neurons and with the phenotypes of the Ret and GDNF knockout animals. Although little expression of GRR3 was found in the brain, it is co-expressed with *ret* and GDNFR- α in the trigeminal ganglia in E18 and P7 rats. These observations indicate that GDNF action may be regulated by association with different binding components depending on the tissue and developmental stage, while always signaling through Ret.

Although expression of *ret* is often co-localized with that of GDNFR- α , GRR2 and GRR3, there are several sites that express one or more of the binding receptors at high levels while *ret* expression is undetectable. Little or no *ret* is expressed in the spleen or lung where all three receptors are expressed at high levels. High levels of GDNFR- α mRNA are found in the liver, medial habenular nucleus, and the hippocampus, and GRR2 expression is prominent in the cortex. Little *ret* expression was observed in either of these regions. The lack of *ret* expression at some sites of substantial GDNFR expression suggests that either a signaling partner other than Ret may be employed by the GDNFRs in these tissues or that the receptors have an alternate mechanism of action. Two possibilities are that the receptors may act to sequester ligands of the GDNF family or that some fraction of

the membrane bound receptors are released and mediate ligand function as soluble receptors.

Experimental Procedures

5

Cloning of GRR3

The GenBank database was searched for sequences related to GDNFR- α and GRR2 using the Wisconsin sequence analysis package (Wisconsin Package Version 9.0, Genetics Computer Group, Madison, WI). Oligonucleotide primers
10 corresponding to regions near the ends of the EST AA238748.Gb_New2 were synthesized. Primers corresponding to AA238748.Gb_New2 were used for PCR screening of 83 pools of 1000 clones each from a rat E15 embryonic cDNA library. A single positive pool was identified by this method. The DNA fragment amplified from this pool was subcloned into a plasmid vector, and the insert was sequenced
15 using an Applied Biosystems 373A automated DNA sequencer with Taq DyeDeoxy Terminator cycle sequencing kits (Applied Biosystems, Foster City, CA). The insert was then labeled with [32 P]-dCTP using a Random Primed DNA Labeling Kit (Stratagene, La Jolla, CA) according to the manufacturer's instructions. Clones from the cDNA library pool that had been identified as positive by PCR were plated on 15
20 cm agarose plates and replicated on duplicate nitrocellulose filters for screening by hybridization to the radiolabeled insert. Filters were prehybridized at 55°C for 3.5 hours in 200 ml of 6 x SSC, 1 x Denhardts, 0.5% SDS, and 50 μ g/ml salmon sperm DNA. Following the addition of 2 x 10⁸ cpm of the radiolabeled probe, hybridization was continued for 18 hours. Filters were then washed twice for 30
25 minutes each at 55°C in 0.2 x SSC, 0.1% SDS and exposed to X-ray film overnight with an intensifying screen.

DNA Sequencing and Sequence Analysis

DNA from clones that screened positively by hybridization was prepared and
30 sequenced using an automated Applied Biosystems 373A DNA sequencer and Taq DyeDeoxy Terminator cycle sequencing kits (Applied Biosystems, Foster City, CA). The peptide sequences of GDNFR- α , GRR2, and GRR3 were aligned using the

Lineup program (Wisconsin Package Version 9.0, Genetics Computer Group, Madison, WI).

Blot Hybridization Analysis

5 For blot hybridization analysis, the cloned rat GRR3 cDNA was labeled using the Random Primed DNA Labeling Kit (Boehringer Mannheim, Indianapolis, IN) according to the manufacturer's instructions. Rat and mouse RNA blots (Clontech) were hybridized with the probe and washed at high stringency using the reagents of the ExpressHyb Kit (Clontech, Palo Alto, CA) according to the
10 instructions of the manufacturer. Following exposure on X-ray film, the filters were stripped of probe by boiling in 0.5% SDS for 10 minutes and rehybridized with a β -actin probe (Clontech, Palo Alto, CA) as a control for total RNA loading.

In situ Hybridization

15 *In situ* hybridization using anti-sense riboprobes of GDNF, *ret*, GDNFR- α , GRR2, and GRR3, was done according to Zhou et al. (Journal Of Neuroscience Research, 37, 129-143, 1994). The *ret* probe is a 316 nt fragment derived from the extracellular domain of the rat *ret* cDNA. GDNF mRNA was detected using a 303 nt fragment of a rat GDNF cDNA clone (nucleotide #50 to 352, Lin et al., 1993).
20 GDNFR- α transcripts were detected with a 396 nt riboprobe (nucleotides 1072 to 1468). GRR2 transcripts were detected with a 205 nt antisense riboprobe corresponding to amino acids 339-413 (Figure 26). GRR3 transcripts were detected with a 225 nt antisense riboprobe corresponding to amino acids 239-315 (Figure 26).

25

While the present invention has been described in terms of preferred embodiments and exemplary nucleic acid and amino acid sequences, it is understood that variations and modifications will occur to those skilled in the art. Therefore, it is intended that the appended claims cover all such equivalent variations which come
30 within the scope of the invention as claimed.

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Fox, Gary M
Jing, Shuqian
Wen, Duanzhi
- (ii) TITLE OF INVENTION: NEUROTROPHIC FACTOR RECEPTORS
- (iii) NUMBER OF SEQUENCES: 44
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: AMGEN INC
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 - (E) COUNTRY: US
 - (F) ZIP: 91320-1789
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/866,354
 - (B) FILING DATE: 30-MAY-1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/837,199
 - (B) FILING DATE: 14-APR-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/015,907
 - (B) FILING DATE: 22-APR-1996
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/017,221
 - (B) FILING DATE: 09-MAY-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Curry, Daniel R.
 - (B) REGISTRATION NUMBER: 32,727
 - (C) REFERENCE/DOCKET NUMBER: A-401B

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2568 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 540..1934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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1 5 10 15	
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CTA AGG CAG TGC GTG GCG GGC AAG GAG ACC AAC TTC AGC CTG GCA TCC	731
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Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu	
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Pro	Cys	Thr	Thr	Ser	Val	Ser	Asn	Asp	Val	Cys	Asn	Arg	Arg	Lys	Cys															
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CAC	AAG	GCC	CTC	CGG	CAG	TTC	TTT	GAC	AAG	GTC	CCG	GCC	AAG	CAC	AGC															1163
His	Lys	Ala	Leu	Arg	Gln	Phe	Phe	Asp	Lys	Val	Pro	Ala	Lys	His	Ser															
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TAC	GGA	ATG	CTC	TTC	TGC	TCC	TGC	CGG	GAC	ATC	GCC	TGC	ACA	GAG	CGG															1211
Tyr	Gly	Met	Leu	Phe	Cys		Cys	Arg	Asp	Ile	Ala	Cys	Thr	Glu	Arg															
	210					215					220																			
AGG	CGA	CAG	ACC	ATC	GTG	CCT	GTG	TGC	TCC	TAT	GAA	GAG	AGG	GAG	AAG															1259
Arg	Arg	Gln	Thr	Ile	Val	Pro	Val	Cys	Ser	Tyr	Glu	Glu	Arg	Glu	Lys															
	225				230					235					240															
CCC	AAC	TGT	TTG	AAT	TTG	CAG	GAC	TCC	TGC	AAG	ACG	AAT	TAC	ATC	TGC															1307
Pro	Asn	Cys	Leu	Asn	Leu	Gln	Asp	Ser	Cys	Lys	Thr	Asn	Tyr	Ile	Cys															
				245				250						255																
AGA	TCT	CGC	CTT	GCG	GAT	TTT	TTT	ACC	AAC	TGC	CAG	CCA	GAG	TCA	AGG															1355
Arg	Ser	Arg	Leu	Ala	Asp	Phe	Phe	Thr	Asn	Cys	Gln	Pro	Glu	Ser	Arg															
			260					265					270																	
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Ser	Val	Ser	Ser	Cys	Leu	Lys	Glu	Asn	Tyr	Ala	Asp	Cys	Leu	Leu	Ala															
		275					280					285																		
TAC	TCG	GGG	CTT	ATT	GGC	ACA	GTC	ATG	ACC	CCC	AAC	TAC	ATA	GAC	TCC															1451
Tyr	Ser	Gly	Leu	Ile	Gly	Thr	Val	Met	Thr	Pro	Asn	Tyr	Ile	Asp	Ser															
	290					295					300																			
AGT	AGC	CTC	AGT	GTG	GCC	CCA	TGG	TGT	GAC	TGC	AGC	AAC	AGT	GGG	AAC															1499
Ser	Ser	Leu	Ser	Val	Ala	Pro	Trp	Cys	Asp	Cys	Ser	Asn	Ser	Gly	Asn															
	305				310					315				320																
GAC	CTA	GAA	GAG	TGC	TTG	AAA	TTT	TTG	AAT	TTC	TTC	AAG	GAC	AAT	ACA															1547
Asp	Leu	Glu	Glu	Cys	Leu	Lys	Phe	Leu	Asn	Phe	Phe	Lys	Asp	Asn	Thr															
				325				330						335																
TGT	CTT	AAA	AAT	GCA	ATT	CAA	GCC	TTT	GGC	AAT	GGC	TCC	GAT	GTG	ACC															1595
Cys	Leu	Lys	Asn	Ala	Ile	Gln	Ala	Phe	Gly	Asn	Gly	Ser	Asp	Val	Thr															
			340				345						350																	
GTG	TGG	CAG	CCA	GCC	TTC	CCA	GTA	CAG	ACC	ACC	ACT	GCC	ACT	ACC	ACC															1643
Val	Trp	Gln	Pro	Ala	Phe	Pro	Val	Gln	Thr	Thr	Thr	Ala	Thr	Thr	Thr															
		355					360					365																		
ACT	GCC	CTC	CGG	GTT	AAG	AAC	AAG	CCC	CTG	GGG	CCA	GCA	GGG	TCT	GAG															1691
Thr	Ala	Leu	Arg	Val	Lys	Asn	Lys	Pro	Leu	Gly	Pro	Ala	Gly	Ser	Glu															
	370					375					380																			
AAT	GAA	ATT	CCC	ACT	CAT	GTT	TTG	CCA	CCG	TGT	GCA	AAT	TTA	CAG	GCA															1739
Asn	Glu	Ile	Pro	Thr	His	Val	Leu	Pro	Pro	Cys	Ala	Asn	Leu	Gln	Ala															
	385				390				395				400																	
CAG	AAG	CTG	AAA	TCC	AAT	GTG	TCG	GGC	AAT	ACA	CAC	CTC	TGT	ATT	TCC															1787
Gln	Lys	Leu	Lys	Ser	Asn	Val	Ser	Gly	Asn	Thr	His	Leu	Cys	Ile	Ser															
				405				410					415																	
AAT	GGT	AAT	TAT	GAA	AAA	GAA	GGT	CTC	GGT	GCT	TCC	AGC	CAC	ATA	ACC															1835
Asn	Gly	Asn	Tyr	Glu	Lys	Glu	Gly	Leu	Gly	Ala	Ser	Ser	His	Ile	Thr															

420	425	430	
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GTC CTG GTG GTA ACC GCT CTG TCC ACC CTA TTA TCT TTA ACA GAA ACA			1931
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Ser			
465			
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(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 465 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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			20					25					30		
Ser	Asp	Gln	Cys	Leu	Lys	Glu	Gln	Ser	Cys	Ser	Thr	Lys	Tyr	Arg	Thr
		35					40					45			
Leu	Arg	Gln	Cys	Val	Ala	Gly	Lys	Glu	Thr	Asn	Phe	Ser	Leu	Ala	Ser
	50					55					60				
Gly	Leu	Glu	Ala	Lys	Asp	Glu	Cys	Arg	Ser	Ala	Met	Glu	Ala	Leu	Lys
65				70				75						80	
Gln	Lys	Ser	Leu	Tyr	Asn	Cys	Arg	Cys	Lys	Arg	Gly	Met	Lys	Lys	Glu
			85					90						95	

Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly
 100 105 110
 Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu
 115 120 125
 Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Asp Val Phe Gln Gln
 130 135 140
 Val Glu His Ile Pro Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala
 145 150 155 160
 Cys Asn Leu Asp Asp Ile Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr
 165 170 175
 Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys Asn Arg Arg Lys Cys
 180 185 190
 His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser
 195 200 205
 Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg
 210 215 220
 Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Lys
 225 230 235 240
 Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys
 245 250 255
 Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg
 260 265 270
 Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala
 275 280 285
 Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser
 290 295 300
 Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn
 305 310 315 320
 Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr
 325 330 335
 Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr
 340 345 350
 Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr
 355 360 365
 Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu
 370 375 380
 Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala
 385 390 395 400
 Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser
 405 410 415
 Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr
 420 425 430
 Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu

435 440 445

Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu Thr
 450 455 460

Ser
 465

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2138 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
- (A) NAME/KEY: CDS
 - (B) LOCATION: 302..1705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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AGCTCGCTCT CCCGGGGCAG TGGTGTGGAT GCACCGGAGT TCGGGCGCTG GGCAAGTTGG      60
GTCGGAAGCTG AACCCCTGAA AGCGGGTCCG CCTCCCGCCC TCGCGCCCGC CCGGATCTGA      120
GTCGCTGGCG GCGGTGGGCG GCAGAGCGAC GGGGAGTCTG CTCTCACCCT GGATGGAGCT      180
GAACTTTGAG TGGCCAGAGG AGCGCAGTCG CCCGGGGATC GCTGCACGCT GAGCTCTCTC      240
CCCGAGACCG GCGGCGGGCT TTGGATTTTG GGGGGGCGGG GACCAGCTGC GCGGCGGCAC      300
C ATG TTC CTA GCC ACT CTG TAC TTC GCG CTG CCA CTC CTG GAT TTG      346
  Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu
    1           5           10           15

CTG ATG TCC GCC GAG GTG AGT GGT GGA GAC CGT CTG GAC TGT GTG AAA      394
Leu Met Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys
           20           25           30

GCC AGC GAT CAG TGC CTG AAG GAA CAG AGC TGC AGC ACC AAG TAC CGC      442
Ala Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg
           35           40           45

ACA CTA AGG CAG TGC GTG GCG GGC AAG GAA ACC AAC TTC AGC CTG ACA      490
Thr Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Thr
           50           55           60

TCC GGC CTT GAG GCC AAG GAT GAG TGC CGT AGC GCC ATG GAG GCC TTG      538
Ser Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu
           65           70           75

AAG CAG AAG TCT CTG TAC AAC TGC CGC TGC AAG CGG GGC ATG AAG AAA      586
Lys Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys
           80           85           90           95

GAG AAG AAT TGT CTG CGT ATC TAC TGG AGC ATG TAC CAG AGC CTG CAG      634
Glu Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln
           100           105           110

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GGA AAT GAC CTC CTG GAA GAT TCC CCG TAT GAG CCG GTT AAC AGC AGG Gly Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg 115 120 125	682
TTG TCA GAT ATA TTC CGG GCA GTC CCG TTC ATA TCA GAT GTT TTC CAG Leu Ser Asp Ile Phe Arg Ala Val Pro Phe Ile Ser Asp Val Phe Gln 130 135 140	730
CAA GTG GAA CAC ATT TCC AAA GGG AAC AAC TGC CTG GAC GCA GCC AAG Gln Val Glu His Ile Ser Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys 145 150 155	778
GCC TGC AAC CTG GAC GAC ACC TGT AAG AAG TAC AGG TCG GCC TAC ATC Ala Cys Asn Leu Asp Asp Thr Cys Lys Lys Tyr Arg Ser Ala Tyr Ile 160 165 170 175	826
ACC CCC TGC ACC ACC AGC ATG TCC AAC GAG GTC TGC AAC CGC CGT AAG Thr Pro Cys Thr Thr Ser Met Ser Asn Glu Val Cys Asn Arg Arg Lys 180 185 190	874
TGC CAC AAG GCC CTC AGG CAG TTC TTC GAC AAG GTT CCG GCC AAG CAC Cys His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His 195 200 205	922
AGC TAC GGG ATG CTC TTC TGC TCC TGC CGG GAC ATC GCC TGC ACC GAG Ser Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu 210 215 220	970
CGG CGG CGA CAG ACT ATC GTC CCC GTG TGC TCC TAT GAA GAA CGA GAG Arg Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu 225 230 235	1018
AGG CCC AAC TGC CTG AGT CTG CAA GAC TCC TGC AAG ACC AAT TAC ATC Arg Pro Asn Cys Leu Ser Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile 240 245 250 255	1066
TGC AGA TCT CGC CTT GCA GAT TTT TTT ACC AAC TGC CAG CCA GAG TCA Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser 260 265 270	1114
AGG TCT GTC AGC AAC TGT CTT AAG GAG AAC TAC GCA GAC TGC CTC CTG Arg Ser Val Ser Asn Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu 275 280 285	1162
GCC TAC TCG GGA CTG ATT GGC ACA GTC ATG ACT CCC AAC TAC GTA GAC Ala Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Val Asp 290 295 300	1210
TCC AGC AGC CTC AGC GTG GCA CCA TGG TGT GAC TGC AGC AAC AGC GGC Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly 305 310 315	1258
AAT GAC CTG GAA GAC TGC TTG AAA TTT CTG AAT TTT TTT AAG GAC AAT Asn Asp Leu Glu Asp Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn 320 325 330 335	1306
ACT TGT CTC AAA AAT GCA ATT CAA GCC TTT GGC AAT GGC TCA GAT GTG Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val 340 345 350	1354
ACC ATG TGG CAG CCA GCC CCT CCA GTC CAG ACC ACC ACT GCC ACC ACT Thr Met Trp Gln Pro Ala Pro Pro Val Gln Thr Thr Thr Ala Thr Thr 355 360 365	1402

ACC ACT GCC TTC CGG GTC AAG AAC AAG CCT CTG GGG CCA GCA GGG TCT 1450
 Thr Thr Ala Phe Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser
 370 375 380

GAG AAT GAG ATC CCC ACA CAC GTT TTA CCA CCC TGT GCG AAT TTG CAG 1498
 Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln
 385 390 395

GCT CAG AAG CTG AAA TCC AAT GTG TCG GGT AGC ACA CAC CTC TGT CTT 1546
 Ala Gln Lys Leu Lys Ser Asn Val Ser Gly Ser Thr His Leu Cys Leu
 400 405 410 415

TCT GAT AGT GAT TTC GGA AAG GAT GGT CTC GCT GGT GCC TCC AGC CAC 1594
 Ser Asp Ser Asp Phe Gly Lys Asp Gly Leu Ala Gly Ala Ser Ser His
 420 425 430

ATA ACC ACA AAA TCA ATG GCT GCT CCT CCC AGC TGC AGT CTG AGC TCA 1642
 Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Ser Leu Ser Ser
 435 440 445

CTG CCG GTG CTG ATG CTC ACC GCC CTT GCT GCC CTG TTA TCT GTA TCG 1690
 Leu Pro Val Leu Met Leu Thr Ala Leu Ala Ala Leu Leu Ser Val Ser
 450 455 460

TTG GCA GAA ACG TCG TAGCTGCATC CGGGAAAACA GTATGAAAAG ACAAAGAGA 1745
 Leu Ala Glu Thr Ser
 465

ACCAAGTATT CTGTCCCTGT CCTCTTGAT ATCTGAAAAT CCAGTTTAA AAGCTCCGTT 1805

GAGAAGCAGT TTCACCCAAC TGGAACCTTT TCCTTGTTTT TAAGAAAGCT TGTGGCCCTC 1865

AGGGGCTTCT GTTGAAGAAC TGCTACAGGG CTAATTCCAA ACCCATAAGG CTCTGGGGCG 1925

TGGTGCGGCT TAAGGGGACC ATTTGCACCA TGTAAGCAA GCTGGGCTTA TCATGTGTTT 1985

GATGGTGAGG ATGGTAGTGG TGATGATGAT GGTAATTTTA ACAGCTTGAA CCCTGTTCTC 2045

TCTACTGGTT AGGAACAGGA GATACTATTG ATAAAGATTC TTCCATGTCT TACTCAGCAG 2105

CATTGCCTTC TGAAGACAGG CCCGCAGCCG TCG 2138

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu
 1 5 10 15

Met Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala
 20 25 30

Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr
 35 40 45

Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Thr Ser

50					55					60					
Gly 65	Leu	Glu	Ala	Lys	Asp 70	Glu	Cys	Arg	Ser	Ala 75	Met	Glu	Ala	Leu	Lys 80
Gln	Lys	Ser	Leu	Tyr 85	Asn	Cys	Arg	Cys	Lys 90	Arg	Gly	Met	Lys	Lys 95	Glu
Lys	Asn	Cys	Leu 100	Arg	Ile	Tyr	Trp	Ser 105	Met	Tyr	Gln	Ser	Leu 110	Gln	Gly
Asn	Asp	Leu 115	Leu	Glu	Asp	Ser	Pro 120	Tyr	Glu	Pro	Val	Asn 125	Ser	Arg	Leu
Ser 130	Asp	Ile	Phe	Arg	Ala	Val 135	Pro	Phe	Ile	Ser	Asp 140	Val	Phe	Gln	Gln
Val 145	Glu	His	Ile	Ser	Lys 150	Gly	Asn	Asn	Cys	Leu 155	Asp	Ala	Ala	Lys	Ala 160
Cys	Asn	Leu	Asp	Asp 165	Thr	Cys	Lys	Lys	Tyr 170	Arg	Ser	Ala	Tyr	Ile 175	Thr
Pro	Cys	Thr 180	Thr	Ser	Met	Ser	Asn 185	Glu	Val	Cys	Asn	Arg 190	Arg	Lys	Cys
His	Lys	Ala 195	Leu	Arg	Gln	Phe	Phe 200	Asp	Lys	Val	Pro 205	Ala	Lys	His	Ser
Tyr 210	Gly	Met	Leu	Phe	Cys 215	Ser	Cys	Arg	Asp	Ile	Ala 220	Cys	Thr	Glu	Arg
Arg 225	Arg	Gln	Thr	Ile	Val 230	Pro	Val	Cys	Ser	Tyr 235	Glu	Glu	Arg	Glu	Arg 240
Pro	Asn	Cys	Leu 245	Ser	Leu	Gln	Asp	Ser	Cys 250	Lys	Thr	Asn	Tyr	Ile 255	Cys
Arg	Ser	Arg 260	Leu	Ala	Asp	Phe	Phe 265	Thr	Asn	Cys	Gln	Pro	Glu 270	Ser	Arg
Ser	Val 275	Ser	Asn	Cys	Leu	Lys	Glu 280	Asn	Tyr	Ala	Asp	Cys 285	Leu	Leu	Ala
Tyr 290	Ser	Gly	Leu	Ile	Gly	Thr 295	Val	Met	Thr	Pro	Asn 300	Tyr	Val	Asp	Ser
Ser 305	Ser	Leu	Ser	Val	Ala 310	Pro	Trp	Cys	Asp	Cys 315	Ser	Asn	Ser	Gly	Asn 320
Asp	Leu	Glu	Asp	Cys 325	Leu	Lys	Phe	Leu	Asn 330	Phe	Phe	Lys	Asp	Asn 335	Thr
Cys	Leu	Lys	Asn 340	Ala	Ile	Gln	Ala	Phe 345	Gly	Asn	Gly	Ser	Asp 350	Val	Thr
Met	Trp	Gln 355	Pro	Ala	Pro	Pro	Val 360	Gln	Thr	Thr	Thr	Ala 365	Thr	Thr	Thr
Thr 370	Ala	Phe	Arg	Val	Lys	Asn 375	Lys	Pro	Leu	Gly	Pro	Ala 380	Gly	Ser	Glu
Asn 385	Glu	Ile	Pro	Thr	His 390	Val	Leu	Pro	Pro	Cys 395	Ala	Asn	Leu	Gln	Ala 400

Gln Lys Leu Lys Ser Asn Val Ser Gly Ser Thr His Leu Cys Leu Ser
 405 410 415
 Asp Ser Asp Phe Gly Lys Asp Gly Leu Ala Gly Ala Ser Ser His Ile
 420 425 430
 Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Ser Leu Ser Ser Leu
 435 440 445
 Pro Val Leu Met Leu Thr Ala Leu Ala Ala Leu Leu Ser Val Ser Leu
 450 455 460
 Ala Glu Thr Ser
 465

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..539
 (D) OTHER INFORMATION: /note= "1 to 539 is -237 to 301 of
 Figure 5 Gdnfr"

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 540..1937

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AATCTGGCCT CGGAACACGC CATTCTCCGC GCCGCTTCCA ATAACCACTA ACATCCCTAA	60
CGAGCATCCG AGCCGAGGGC TCTGCTCGGA AATCGTCCTG GCCCAACTCG GCCCTTCGAG	120
CTCTCGAAGA TTACCGCATC TATTTTTTTT TTCTTTTTTT TCTTTTCCTA GCGCAGATAA	180
AGTGAGCCCG GAAAGGGAAG GAGGGGGCGG GGACACCATT GCCCTGAAAG AATAAATAAG	240
TAAATAAACA AACTGGCTCC TCGCCGCAGC TGGACGCGGT CGGTTGAGTC CAGGTTGGGT	300
CGGACCTGAA CCCCTAAAAG CGGAACCGCC TCCCGCCCTC GCCATCCCGG AGCTGAGTCG	360
CCGGCGGCGG TGGCTGCTGC CAGACCCGGA GTTTCCTCTT TCACTGGATG GAGCTGAACT	420
TTGGGCGGCC AGAGCAGCAC AGCTGTCCGG GGATCGCTGC ACGCTGAGCT CCCTCGGCAA	480
GACCCAGCGG CGGCTCGGGA TTTTTTTGGG GGGGCGGGGA CCAGCCCCGC GCCGGCACC	539
ATG TTC CTG GCG ACC CTG TAC TTC GCG CTG CCG CTC TTG GAC TTG CTC	587
Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu	
1 5 10 15	
CTG TCG GCC GAA GTG AGC GGC GGA GAC CGC CTG GAT TGC GTG AAA GCC	635
Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala	

20										25										30											
AGT	GAT	CAG	TGC	CTG	AAG	GAG	CAG	AGC	TGC	AGC	ACC	AAG	TAC	CGC	ACG															683	
Ser	Asp	Gln	Cys	Leu	Lys	Glu	Gln	Ser	Cys	Ser	Thr	Lys	Tyr	Arg	Thr																
		35					40					45																			
CTA	AGG	CAG	TGC	GTG	GCG	GGC	AAG	GAG	ACC	AAC	TTC	AGC	CTG	GCA	TCC															731	
Leu	Arg	Gln	Cys	Val	Ala	Gly	Lys	Glu	Thr	Asn	Phe	Ser	Leu	Ala	Ser																
		50				55					60																				
GGC	CTG	GAG	GCC	AAG	GAT	GAG	TGC	CGC	AGC	GCC	ATG	GAG	GCC	CTG	AAG															779	
Gly	Leu	Glu	Ala	Lys	Asp	Glu	Cys	Arg	Ser	Ala	Met	Glu	Ala	Leu	Lys																
		65			70					75					80																
CAG	AAG	TCG	CTC	TAC	AAC	TGC	CGC	TGC	AAG	CGG	GGT	ATG	AAG	AAG	GAG															827	
Gln	Lys	Ser	Leu	Tyr	Asn	Cys	Arg	Cys	Lys	Arg	Gly	Met	Lys	Lys	Glu																
				85					90					95																	
AAG	AAC	TGC	CTG	CGC	ATT	TAC	TGG	AGC	ATG	TAC	CAG	AGC	CTG	CAG	GGA															875	
Lys	Asn	Cys	Leu	Arg	Ile	Tyr	Trp	Ser	Met	Tyr	Gln	Ser	Leu	Gln	Gly																
			100					105					110																		
AAT	GAT	CTG	CTG	GAG	GAT	TCC	CCA	TAT	GAA	CCA	GTT	AAC	AGC	AGA	TTG															923	
Asn	Asp	Leu	Leu	Glu	Asp	Ser	Pro	Tyr	Glu	Pro	Val	Asn	Ser	Arg	Leu																
		115				120					125																				
TCA	GAT	ATA	TTC	CGG	GTG	GTC	CCA	TTC	ATA	TCA	GAT	GTT	TTT	CAG	CAA															971	
Ser	Asp	Ile	Phe	Arg	Val	Val	Pro	Phe	Ile	Ser	Asp	Val	Phe	Gln	Gln																
		130				135					140																				
GTG	GAG	CAC	ATT	CCC	AAA	GGG	AAC	AAC	TGC	CTG	GAT	GCA	GCG	AAG	GCC															1019	
Val	Glu	His	Ile	Pro	Lys	Gly	Asn	Asn	Cys	Leu	Asp	Ala	Ala	Lys	Ala																
		145			150				155					160																	
TGC	AAC	CTC	GAC	GAC	ATT	TGC	AAG	AAG	TAC	AGG	TCG	GCG	TAC	ATC	ACC															1067	
Cys	Asn	Leu	Asp	Asp	Ile	Cys	Lys	Lys	Tyr	Arg	Ser	Ala	Tyr	Ile	Thr																
				165					170					175																	
CCG	TGC	ACC	ACC	AGC	GTG	TCC	AAN	GAT	GTC	TGC	AAC	CGC	CGC	AAG	TGC															1115	
Pro	Cys	Thr	Thr	Ser	Val	Ser	Xaa	Asp	Val	Cys	Asn	Arg	Arg	Lys	Cys																
			180				185					190																			
CAC	AAG	GCC	CTC	CGG	CAG	TTC	TTT	GAC	AAG	GTC	CCG	GCC	AAG	CAC	AGC															1163	
His	Lys	Ala	Leu	Arg	Gln	Phe	Phe	Asp	Lys	Val	Pro	Ala	Lys	His	Ser																
		195				200					205																				
TAC	GGA	ATG	CTC	TTC	TGC	TCC	TGC	CGG	GAC	ATC	GCC	TGC	ACA	GAG	CGG															1211	
Tyr	Gly	Met	Leu	Phe	Cys	Ser	Cys	Arg	Asp	Ile	Ala	Cys	Thr	Glu	Arg																
		210				215					220																				
AGG	CGA	CAG	ACC	ATC	GTG	CCT	GTG	TGC	TCC	TAT	GAA	GAG	AGG	GAG	AAG															1259	
Arg	Arg	Gln	Thr	Ile	Val	Pro	Val	Cys	Ser	Tyr	Glu	Glu	Arg	Glu	Lys																
		225			230					235					240																
CCC	AAC	TGT	TTG	AAT	TTG	CAG	GAC	TCC	TGC	AAG	ACG	AAT	TAC	ATC	TGC															1307	
Pro	Asn	Cys	Leu	Asn	Leu	Gln	Asp	Ser	Cys	Lys	Thr	Asn	Tyr	Ile	Cys																
				245					250					255																	
AGA	TCT	CGC	CTT	GCG	GAT	TTT	TTT	ACC	AAC	TGC	CAG	CCA	GAG	TCA	AGG															1355	
Arg	Ser	Arg	Leu	Ala	Asp	Phe	Phe	Thr	Asn	Cys	Gln	Pro	Glu	Ser	Arg																
			260					265					270																		
TCT	GTC	AGC	AGC	TGT	CTA	AAG	GAA	AAC	TAC	GCT	GAC	TGC	CTC	CTC	GCC															1403	
Ser	Val	Ser	Ser	Cys	Leu	Lys	Glu	Asn	Tyr	Ala	Asp	Cys	Leu	Leu	Ala																

275	280	285	
TAC TCG GGG CTT ATT GGC ACA GTC ATG ACC CCC AAC TAC ATA GAC TCC Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser 290 295 300			1451
AGT AGC CTC AGT GTG GCC CCA TGG TGT GAC TGC AGC AAC AGT GGG AAC Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn 305 310 315 320			1499
GAC CTA GAA GAG TGC TTG AAA TTT TTG AAT TTC TTC AAG GAC AAT ACA Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr 325 330 335			1547
TGT CTT AAA AAT GCA ATT CAA GCC TTT GGC AAT GGC TCC GAT GTG ACC Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr 340 345 350			1595
GTG TGG CAG CCA GCC TTC CCA GTA CAG ACC ACC ACT GCC ACT ACC ACC Val Trp Gln Pro Ala Phe Pro Gln Thr Thr Thr Ala Thr Thr Thr 355 360 365			1643
ACT GCC CTC CGG GTT AAG AAC AAG CCC CTG GGG CCA GCA GGG TCT GAG Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu 370 375 380			1691
AAT GAA ATT CCC ACT CAT GTT TTG CCA CCG TGT GCA AAT TTA CAG GCA Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala 385 390 395 400			1739
CAG AAG CTG AAA TCC AAT GTG TCG GGC AAT ACA CAC CTC TGT ATT TCC Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser 405 410 415			1787
AAT GGT AAT TAT GAA AAA GAA GGT CTC GGT GCT TCC AGC CAC ATA ACC Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr 420 425 430			1835
ACA AAA TCA ATG GCT GCT CCT CCA AGC TGT GGT CTG AGC CCA CTG CTG Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu 435 440 445			1883
GTC CTG GTG GTA ACC GCT CTG TCC ACC CTA TTA TCT TTA ACA GAA ACA Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu Thr 450 455 460			1931
TCA TAG CTGCATTAAA AAAATACAAT ATGGACATGT AAAAAGACAA AAACCAAGTT Ser * 465			1987
ATCTGTTTCC TGTTCCTTG TATAGCTGAA ATTCCAGTTT AGGAGCTCAG TTGAGAAACA			2047
GTTCCATTCA ACTGGAACAT TTTTTTTTTT NCCTTTTAAG AAAGCTTCTT GTGATCCTTC			2107
GGGGCTTCTG TGAAAAACCT GATGCAGTGC TCCATCCAAA CTCAGAAGGC TTTGGGATAT			2167
GCTGTATTTT AAAGGGACAG TTTGTAACCT GGGCTGTAAA GCAAAGTGGG GCTGTGTTTT			2227
CGATGATGAT GATCATCATG ATCATGATNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN			2287
NNNNNNNGAT TTAAACAGTT TTACTTCTGG CCTTTCCTAG CTAGAGAAGG AGTTAATATT			2347
TCTAAGGTAA CTCCCATATC TCCTTTAATG ACATTGATTT CTAATGATAT AAATTTTCAGC			2407

CTACATTGAT GCCAAGCTTT TTTGCCACAA AGAAGATTCT TACCAAGAGT GGGCTTTGTG 2467
 GAAACAGCTG GTACTGATGT TCACCTTTAT ATATGTACTA GCATTTTCCA CGCTGATGTT 2527
 TATGTACTGT AAACAGTTCT GCACTCTTGT ACAAAGAAA AAACACCTGT CACATCCAAA 2587
 TATAGTATCT GTCTTTTCGT CAAAATAGAG AGTGGGGAAT GAGTGTGCCG ATTCAATACC 2647
 TCAATCCCTG AACGACACTC TCCTAATCCT AAGCCTTACC TGAGTGAGAA GCCCTTTACC 2707
 TAACAAAAGT CCAATATAGC TGAAATGTCG CTCTAATACT CTTTACACAT ATGAGGTTAT 2767
 ATGTAGAAAA AAATTTTACT ACTAAATGAT TTCAACTATT GGCTTTCTAT ATTTTGAAAG 2827
 TAATGATATT GTCTCATTTT TTTACTGATG GTTTAATACA AAATACACAG AGCTTGTTTC 2887
 CCCTCATAAG TAGTGTTTCG TCTGATATGA ACTTCACAAA TACAGCTCAT CAAAAGCAGA 2947
 CTCTGAGAAG CCTCGTGCTG TAGCAGAAAAG TTCTGCATCA TGTGACTGTG GACAGGCAGG 3007
 AGGAAACAGA ACAGACAAGC ATTGTCTTTT GTCATTGCTC GAAGTGCAAG CGTGCATACC 3067
 TGTGGAGGGA ACTGGTGGCT GCTTGTAAT GTTCTGCAGC ATCTCTTGAC ACACTTGTC A 3127
 TGACACAATC CAGTACCTTG GTTTTCAGGT TATCTGACAA AGGCAGCTTT GATTGGGACA 3187
 TGGAGGCATG GGCAGGCCGG AA 3209

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu
 1 5 10 15
 Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala
 20 25 30
 Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr
 35 40 45
 Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser
 50 55 60
 Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys
 65 70 75 80
 Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu
 85 90 95
 Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly
 100 105 110
 Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu
 115 120 125

Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Asp Val Phe Gln Gln
 130 135 140
 Val Glu His Ile Pro Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala
 145 150 155 160
 Cys Asn Leu Asp Asp Ile Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr
 165 170 175
 Pro Cys Thr Thr Ser Val Ser Xaa Asp Val Cys Asn Arg Arg Lys Cys
 180 185 190
 His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser
 195 200 205
 Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg
 210 215 220
 Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Lys
 225 230 235 240
 Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys
 245 250 255
 Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg
 260 265 270
 Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala
 275 280 285
 Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser
 290 295 300
 Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn
 305 310 315 320
 Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr
 325 330 335
 Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr
 340 345 350
 Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr
 355 360 365
 Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu
 370 375 380
 Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala
 385 390 395 400
 Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser
 405 410 415
 Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr
 420 425 430
 Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu
 435 440 445
 Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu Thr
 450 455 460
 Ser *

465

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..508
- (D) OTHER INFORMATION: /note= "1 to 508 is -237 to 272 of Figure 5 Hsgr-21af"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
TCTGGCCTCG GAACACGCCA TTCTCCGCGC CGCTTCCAAT AACCCTAAC ATCCCTAACG      60
AGCATCCGAG CCGAGGGCTC TGCTCGGAAA TCGTCTGGC CCAACTCGGC CCTTCGAGCT      120
CTCGAAGATT ACCGCATCTA TTTTTTTTTT CTTTTTTTTC TTTTCCTAGC GCAGATAAAG      180
TGAGCCCGGA AAGGGAAGGA GGGGGCGGGG ACACCATTCG CCTGAAAGAA TAAATAAGTA      240
AATAAACAAA CTGGCTCCTC GCCGCAGCTG GACGCGGTCG GTTGAGTCCA GGTTGGGTCTG      300
GACCTGAACC CCTAAAAGCG GAACCGCCTC CCGCCCTCGC CATCCCGGAG CTGAGTCGCC      360
GGCGGCGGTG GCTGCTGCCA GACCCGGAGT TTCCTCTTTC ACTGGATGGA GCTGAACTTT      420
GGGCGGCCAG AGCAGCACAG CTGTCCGGGG ATCGCTGCAC GCTGAGCTCC CTCGGCAAGA      480
CCCAGCGGCG GCTCGGGATT TTTTGGG                                     508
```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 510 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..510
- (D) OTHER INFORMATION: /note= "1 to 510 is -237 to 272 of Figure 5 Hsgr-21bf"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
AATCTGGCCT CGGAACACGC CATTCTCCGC GCCGCTTCCA ATAACCACTA ACATCCCTAA      60
CGAGCATCCG AGCCGAGGGC TCTGCTCGGA AATCGTCCTG GCCCAACTCG GCCCTTCGAG      120
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CTCTCGAAGA TTACCGCATC TATTTTTTTT TTCTTTTTTT TCTTTTCCTA GCGCAGATAA      180
AGTGAGCCCG GAAAGGGAAG GAGGGGGCGG GGACACCATT GCCCTGAAAG AATAAATAAG      240
TAAATAAACA AACTGGCTCC TCGCCGCAGC TGGACGCGGT CGGTTGAGTC CAGGTTGGGT      300
CGGACCTGAA CCCCTAAAAG CGGAACCGCC TCCCGCCCTC GCCATCCCGG AGCTGAGTCG      360
CCGGCGGCGG TGGCTGCTGC CAGACCCGGA GTTTCCTCTT TCACTGGATG GAGCTGAACT      420
TTGGGCGGCC AGAGCAGCAC AGCTGTCCGG GGATCGCTGC ACGCTGAGCT CCCTCGGCAA      480
GACCCAGCGG CGGCTCGGGA TTTTTTTGGG      510

```

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1927 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 538..1926

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..537

(D) OTHER INFORMATION: /note= "1 to 537 is -235 to 301 of Figure 5 21acon"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```

TCTGGCCTCG GAACACGCCA TTCTCCGCGC CGCTTCCAAT AACCATAAC ATCCCTAACG      60
AGCATCCGAG CCGAGGGCTC TGCTCGGAAA TCGTCCTGGC CCAACTCGGC CCTTCGAGCT      120
CTCGAAGATT ACCGCATCTA TTTTTTTTTT CTTTTTTTTC TTTTCCTAGC GCAGATAAAG      180
TGAGCCCGGA AAGGGAAGGA GGGGGCGGGG ACACCATTCG CCTGAAAGAA TAAATAAGTA      240
AATAAACAAA CTGGCTCCTC GCCGCAGCTG GACGCGGTCTG GTTGAGTCCA GGTGGGGTCG      300
GACCTGAACC CTTAAAAGCG GAACCGCCTC CCGCCCTCGC CATCCCGGAG CTGAGTCGCC      360
GGCGGCGGTG GCTGCTGCCA GACCCGGAGT TTCCTCTTTC ACTGGATGGA GCTGAACTTT      420
GGGCGGCCAG AGCAGCACAG CTGTCCGGGG ATCGCTGCAC GCTGAGCTCC CTCGGCAAGA      480
CCCAGCGGCG GCTCGGGATT TTTTGGGGG GCGGGGACC AGCCCCGCGC CGGCACC      537
ATG TTC CTG GCG NCC CTG TAC TTC GCG CTG CCG CTC TTG GAC TTG CTC      585
Met Phe Leu Ala Xaa Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu
  1           5           10           15
CTG TCG GCC GAA GTG AGC GGC GGA GAC CGC CTG GAT TGC GTG AAA GCC      633
Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala
          20           25           30

```


AGT GAT CAG TGC CTG AAG GAG CAG AGC TGC AGC ACC AAG TAC CGC ACG Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr 35 40 45	681
CTA AGG CAG TGC GTG GCG GGC AAG GAG ACC AAC TTC AGC CTG GCA TCC Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser 50 55 60	729
GGC CTG GAG GCC AAG GAT GAG TGC CGC AGC GCC ATG GAG GCC CTG AAG Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys 65 70 75 80	777
CAG AAG TCG CTC TAC AAC TGC CGC TGC AAG CGG GGT ATG AAG AAG GAG Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu 85 90 95	825
AAG AAC TGC CTG CGC ATT TAC TGG AGC ATG TAC CAG AGC CTG CAG GGA Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly 100 105 110	873
AAT GAT CTG CTG GAG GAT TCC CCA TAT GAA CCA GTT AAC AGC AGA TTG Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu 115 120 125	921
TCA GAT ATA TTC CGG GTG GTC CCA TTC ATA TCA GAT GTT TTT CAG CAA Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Asp Val Phe Gln Gln 130 135 140	969
GTG GAG CAC ATT CCC AAA GGG AAC AAC TGC CTG GAT GCA GCG AAG GCC Val Glu His Ile Pro Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala 145 150 155 160	1017
TGC AAC CTC GAC GAC ATT TGC AAG AAG TAC AGG TCG GCG TAC ATC ACC Cys Asn Leu Asp Asp Ile Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr 165 170 175	1065
CCG TGC ACC ACC AGC GTG TCC AAC GAT GTC TGC AAC CGC CGC AAG TGC Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys Asn Arg Arg Lys Cys 180 185 190	1113
CAC AAG GCC CTC CGG CAG TTC TTT GAC AAG GTC CCG GCC AAG CAC AGC His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser 195 200 205	1161
TAC GGA ATG CTC TTC TGC TCC TGC CGG GAC ATC GCC TGC ACA GAG CGG Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg 210 215 220	1209
AGG CGA CAG ACC ATC GTG CCT GTG TGC TCC TAT GAA GAG AGG GAG AAG Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Lys 225 230 235 240	1257
CCC AAC TGT TTG AAT TTG CAG GAC TCC TGC AAG ACG AAT TAC ATC TGC Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys 245 250 255	1305
AGA TCT CGC CTT GCG GAT TTT TTT ACC AAC TGC CAG CCA GAG TCA AGG Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg 260 265 270	1353
TCT GTC AGC AGC TGT CTA AAG GAA AAC TAC GCT GAC TGC CTC CTC GCC Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala 275 280 285	1401

TAC TCG GGG CTT ATT GGC ACA GTC ATG ACC CCC AAC TAC ATA GAC TCC	1449
Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser	
290 295 300	
AGT AGC CTC AGT GTG GCC CCA TGG TGT GAC TGC AGC AAC AGT GGG AAC	1497
Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn	
305 310 315 320	
GAC CTA GAA GAG TGC TTG AAA TTT TTG AAT TTC TTC AAG GAC AAT ACA	1545
Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr	
325 330 335	
TGT CTT AAA AAT GCA ATT CAA GCC TTT GGC AAT GGC TCC GAT GTG ACC	1593
Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr	
340 345 350	
GTG TGG CAG CCA GCC TTC CCA GTA CAG ACC ACC ACT GCC ACT ACC ACC	1641
Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr	
355 360 365	
ACT GCC CTC CGG GTT AAG AAC AAG CCC CTG GGG CCA GCA GGG TCT GAG	1689
Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu	
370 375 380	
AAT GAA ATT CCC ACT CAT GTT TTG CCA CCG TGT GCA AAT TTA CAG GCA	1737
Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala	
385 390 395 400	
CAG AAG CTG AAA TCC AAT GTG TCG GGC AAT ACA CAC CTC TGT ATT TCC	1785
Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser	
405 410 415	
AAT GGT AAT TAT GAA AAA GAA GGT CTC GGT GCT TCC AGC CAC ATA ACC	1833
Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr	
420 425 430	
ACA AAA TCA ATG GCT GCT CCT CCA AGC TGT GGT CTG AGC CCA CTG CTG	1881
Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu	
435 440 445	
GTC CTG GTG GTA ACC GCT CTG TCC ACC CTA TTA TCT TTA ACA GAA	1926
Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu	
450 455 460	
A	1927

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Phe Leu Ala Xaa Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu
1 5 10 15
Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala
20 25 30

Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr
 35 40 45
 Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser
 50 55 60
 Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys
 65 70 75 80
 Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu
 85 90 95
 Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly
 100 105 110
 Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu
 115 120 125
 Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Asp Val Phe Gln Gln
 130 135 140
 Val Glu His Ile Pro Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala
 145 150 155 160
 Cys Asn Leu Asp Asp Ile Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr
 165 170 175
 Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys Asn Arg Arg Lys Cys
 180 185 190
 His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser
 195 200 205
 Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg
 210 215 220
 Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Lys
 225 230 235 240
 Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys
 245 250 255
 Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg
 260 265 270
 Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala
 275 280 285
 Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser
 290 295 300
 Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn
 305 310 315 320
 Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr
 325 330 335
 Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr
 340 345 350
 Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr
 355 360 365
 Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu

370	375	380
Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala		
385	390	395 400
Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser		
	405	410 415
Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr		
	420	425 430
Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu		
	435	440 445
Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu		
	450	455 460

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1929 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 540..1928

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..539

(D) OTHER INFORMATION: /note= "1 to 539 is -237 to 301 of Figure 5 21bcon"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AATCTGGCCT CGGAACACGC CATTCTCCGC GCCGCTTCCA ATAACCACTA ACATCCCTAA	60
CGAGCATCCG AGCCGAGGGC TCTGCTCGGA AATCGTCCTG GCCCAACTCG GCCCTTCGAG	120
CTCTCGAAGA TTACCGCATC TATTTTTTTTT TTCTTTTTTT TCTTTTCCTA GCGCAGATAA	180
AGTGAGCCCG GAAAGGGAAG GAGGGGGCGG GGACACCATT GCCCTGAAAG AATAAATAAG	240
TAAATAAACA AACTGGCTCC TCGCCGCAGC TGGACGCGGT CGGTTGAGTC CAGGTTGGGT	300
CGGACCTGAA CCCCTAAAAG CGGAACCGCC TCCCGCCCTC GCCATCCCGG AGCTGAGTCG	360
CCGGCGGCGG TGGCTGCTGC CAGACCCGGA GTTTCCTCTT TCACTGGATG GAGCTGAACT	420
TTGGGCGGCC AGAGCAGCAC AGCTGTCCGG GGATCGCTGC ACGCTGAGCT CCCTCGGCAA	480
GACCCAGCGG CGGCTCGGGA TTTTTTTGGG GGGGCGGGGA CCAGCCCCGC GCCGGCACC	539
ATG TTC CTG GCG ACC CTG TAC TTC GCG CTG CCG CTC TTG GAC TTG CTC	587
Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu	
1 5 10 15	
CTG TCG GCC GAA GTG AGC GGC GGA GAC CGC CTG GAT TGC GTG AAA GCC	635

Leu	Ser	Ala	Glu	Val	Ser	Gly	Gly	Asp	Arg	Leu	Asp	Cys	Val	Lys	Ala		
			20					25					30				
AGT	GAT	CAG	TGC	CTG	AAG	GAG	CAG	AGC	TGC	AGC	ACC	AAG	TAC	CGC	ACG		683
Ser	Asp	Gln	Cys	Leu	Lys	Glu	Gln	Ser	Cys	Ser	Thr	Lys	Tyr	Arg	Thr		
		35					40					45					
CTA	AGG	CAG	TGC	GTG	GCG	GGC	AAG	GAG	ACC	AAC	TTC	AGC	CTG	GCA	TCC		731
Leu	Arg	Gln	Cys	Val	Ala	Gly	Lys	Glu	Thr	Asn	Phe	Ser	Leu	Ala	Ser		
	50					55					60						
GGC	CTG	GAG	GCC	AAG	GAT	GAG	TGC	CGC	AGC	GCC	ATG	GAG	GCC	CTG	AAG		779
Gly	Leu	Glu	Ala	Lys	Asp	Glu	Cys	Arg	Ser	Ala	Met	Glu	Ala	Leu	Lys		
	65				70					75					80		
CAG	AAG	TCG	CTC	TAC	AAC	TGC	CGC	TGC	AAG	CGG	GGT	ATG	AAG	AAG	GAG		827
Gln	Lys	Ser	Leu	Tyr	Asn	Cys	Arg	Cys	Lys	Arg	Gly	Met	Lys	Lys	Glu		
				85					90					95			
AAG	AAC	TGC	CTG	CGC	ATT	TAC	TGG	AGC	ATG	TAC	CAG	AGC	CTG	CAG	GGA		875
Lys	Asn	Cys	Leu	Arg	Ile	Tyr	Trp	Ser	Met	Tyr	Gln	Ser	Leu	Gln	Gly		
			100					105					110				
AAT	GAT	CTG	CTG	GAG	GAT	TCC	CCA	TAT	GAA	CCA	GTT	AAC	AGC	AGA	TTG		923
Asn	Asp	Leu	Leu	Glu	Asp	Ser	Pro	Tyr	Glu	Pro	Val	Asn	Ser	Arg	Leu		
		115					120					125					
TCA	GAT	ATA	TTC	CGG	GTG	GTC	CCA	TTC	ATA	TCA	GAT	GTT	TTT	CAG	CAA		971
Ser	Asp	Ile	Phe	Arg	Val	Val	Pro	Phe	Ile	Ser	Asp	Val	Phe	Gln	Gln		
	130					135					140						
GTG	GAG	CAC	ATT	CCC	AAA	GGG	AAC	AAC	TGC	CTG	GAT	GCA	GCG	AAG	GCC		1019
Val	Glu	His	Ile	Pro	Lys	Gly	Asn	Asn	Cys	Leu	Asp	Ala	Ala	Lys	Ala		
	145				150				155						160		
TGC	AAC	CTC	GAC	GAC	ATT	TGC	AAG	AAG	TAC	AGG	TCG	GCG	TAC	ATC	ACC		1067
Cys	Asn	Leu	Asp	Asp	Ile	Cys	Lys	Lys	Tyr	Arg	Ser	Ala	Tyr	Ile	Thr		
				165					170					175			
CCG	TGC	ACC	ACC	AGC	GTG	TCC	AAC	GAT	GTC	TGC	AAC	CGC	CGC	AAG	TGC		1115
Pro	Cys	Thr	Thr	Ser	Val	Ser	Asn	Asp	Val	Cys	Asn	Arg	Arg	Lys	Cys		
			180					185					190				
CAC	AAG	GCC	CTC	CGG	CAG	TTC	TTT	GAC	AAG	GTC	CCG	GCC	AAG	CAC	AGC		1163
His	Lys	Ala	Leu	Arg	Gln	Phe	Phe	Asp	Lys	Val	Pro	Ala	Lys	His	Ser		
		195				200						205					
TAC	GGA	ATG	CTC	TTC	TGC	TCC	TGC	CGG	GAC	ATC	GCC	TGC	ACA	GAG	CGG		1211
Tyr	Gly	Met	Leu	Phe	Cys	Ser	Cys	Arg	Asp	Ile	Ala	Cys	Thr	Glu	Arg		
	210				215					220							
AGG	CGA	CAG	ACC	ATC	GTG	CCT	GTG	TGC	TCC	TAT	GAA	GAG	AGG	GAG	AAG		1259
Arg	Arg	Gln	Thr	Ile	Val	Pro	Val	Cys	Ser	Tyr	Glu	Glu	Arg	Glu	Lys		
	225				230					235					240		
CCC	AAC	TGT	TTG	AAT	TTG	CAG	GAC	TCC	TGC	AAG	ACG	AAT	TAC	ATC	TGC		1307
Pro	Asn	Cys	Leu	Asn	Leu	Gln	Asp	Ser	Cys	Lys	Thr	Asn	Tyr	Ile	Cys		
				245					250					255			
AGA	TCT	CGC	CTT	GCG	GAT	TTT	TTT	ACC	AAC	TGC	CAG	CCA	GAG	TCA	AGG		1355
Arg	Ser	Arg	Leu	Ala	Asp	Phe	Phe	Thr	Asn	Cys	Gln	Pro	Glu	Ser	Arg		
			260					265					270				
TCT	GTC	AGC	AGC	TGT	CTA	AAG	GAA	AAC	TAC	GCT	GAC	TGC	CTC	CTC	GCC		1403

Ser	Val	Ser	Ser	Cys	Leu	Lys	Glu	Asn	Tyr	Ala	Asp	Cys	Leu	Leu	Ala		
	275						280					285					
TAC	TCG	GGG	CTT	ATT	GGC	ACA	GTC	ATG	ACC	CCC	AAC	TAC	ATA	GAC	TCC	1451	
Tyr	Ser	Gly	Leu	Ile	Gly	Thr	Val	Met	Thr	Pro	Asn	Tyr	Ile	Asp	Ser		
	290					295					300						
AGT	AGC	CTC	AGT	GTG	GCC	CCA	TGG	TGT	GAC	TGC	AGC	AAC	AGT	GGG	AAC	1499	
Ser	Ser	Leu	Ser	Val	Ala	Pro	Trp	Cys	Asp	Cys	Ser	Asn	Ser	Gly	Asn		
	305				310					315				320			
GAC	CTA	GAA	GAG	TGC	TTG	AAA	TTT	TTG	AAT	TTC	TTC	AAG	GAC	AAT	ACA	1547	
Asp	Leu	Glu	Glu	Cys	Leu	Lys	Phe	Leu	Asn	Phe	Phe	Lys	Asp	Asn	Thr		
				325					330					335			
TGT	CTT	AAA	AAT	GCA	ATT	CAA	GCC	TTT	GGC	AAT	GGC	TCC	GAT	GTG	ACC	1595	
Cys	Leu	Lys	Asn	Ala	Ile	Gln	Ala	Phe	Gly	Asn	Gly	Ser	Asp	Val	Thr		
			340					345					350				
GTG	TGG	CAG	CCA	GCC	TTC	CCA	GTA	CAG	ACC	ACC	ACT	GCC	ACT	ACC	ACC	1643	
Val	Trp	Gln	Pro	Ala	Phe	Pro	Val	Gln	Thr	Thr	Thr		Ala	Thr	Thr		
		355					360						365				
ACT	GCC	CTC	CGG	GTT	AAG	AAC	AAG	CCC	CTG	GGG	CCA	GCA	GGG	TCT	GAG	1691	
Thr	Ala	Leu	Arg	Val	Lys	Asn	Lys	Pro	Leu	Gly	Pro	Ala	Gly	Ser	Glu		
	370					375					380						
AAT	GAA	ATT	CCC	ACT	CAT	GTT	TTG	CCA	CCG	TGT	GCA	AAT	TTA	CAG	GCA	1739	
Asn	Glu	Ile	Pro	Thr	His	Val	Leu	Pro	Pro	Cys	Ala	Asn	Leu	Gln	Ala		
	385				390					395				400			
CAG	AAG	CTG	AAA	TCC	AAT	GTG	TCG	GGC	AAT	ACA	CAC	CTC	TGT	ATT	TCC	1787	
Gln	Lys	Leu	Lys	Ser	Asn	Val	Ser	Gly	Asn	Thr	His	Leu	Cys	Ile	Ser		
			405					410					415				
AAT	GGT	AAT	TAT	GAA	AAA	GAA	GGT	CTC	GGT	GCT	TCC	AGC	CAC	ATA	ACC	1835	
Asn	Gly	Asn	Tyr	Glu	Lys	Glu	Gly	Leu	Gly	Ala	Ser	Ser	His	Ile	Thr		
		420					425						430				
ACA	AAA	TCA	ATG	GCT	GCT	CCT	CCA	AGC	TGT	GGT	CTG	AGC	CCA	CTG	CTG	1883	
Thr	Lys	Ser	Met	Ala	Ala	Pro	Pro	Ser	Cys	Gly	Leu	Ser	Pro	Leu	Leu		
		435					440					445					
GTC	CTG	GTG	GTA	ACC	GCT	CTG	TCC	ACC	CTA	TTA	TCT	TTA	ACA	GAA		1928	
Val	Leu	Val	Val	Thr	Ala	Leu	Ser	Thr	Leu	Leu	Ser	Leu	Thr	Glu			
	450					455					460						
A																1929	

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Phe	Leu	Ala	Thr	Leu	Tyr	Phe	Ala	Leu	Pro	Leu	Leu	Asp	Leu	Leu
1				5					10					15	

Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala
 20 25 30
 Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr
 35 40 45
 Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser
 50 55 60
 Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys
 65 70 75 80
 Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu
 85 90 95
 Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly
 100 105 110
 Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu
 115 120 125
 Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Asp Val Phe Gln Gln
 130 135 140
 Val Glu His Ile Pro Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala
 145 150 155 160
 Cys Asn Leu Asp Asp Ile Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr
 165 170 175
 Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys Asn Arg Arg Lys Cys
 180 185 190
 His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser
 195 200 205
 Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg
 210 215 220
 Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Lys
 225 230 235 240
 Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys
 245 250 255
 Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg
 260 265 270
 Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala
 275 280 285
 Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser
 290 295 300
 Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn
 305 310 315 320
 Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr
 325 330 335
 Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr
 340 345 350
 Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr

355	360	365
Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu		
370	375	380
Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala		
385	390	395 400
Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser		
	405	410 415
Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr		
	420	425 430
Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu		
	435	440 445
Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu		
	450	455 460

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..699
- (D) OTHER INFORMATION: /note= "1 to 699 is 814 to 1512 of

Figure 5 Hsgr-29a"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

G TCG GCG TAC ATC ACC CCG TGC ACC ACC AGC GTG TCC AAT GAT GTC	46
Ser Ala Tyr Ile Thr Pro Cys Thr Thr Ser Val Ser Asn Asp Val	
1 5 10 15	
TGC AAC CGC CGC AAG TGC CAC AAG GCC CTC CGG CAG TTC TTT GAC AAG	94
Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Lys	
20 25 30	
GTC CCG GCC AAG CAC AGC TAC GGA ATG CTC TTC TGC TCC TGC CGG GAC	142
Val Pro Ala Lys His Ser Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp	
35 40 45	
ATC GCC TGC ACA GAG CGG AGG CGA CAG ACC ATC GTG CCT GTG TGC TCC	190
Ile Ala Cys Thr Glu Arg Arg Arg Gln Thr Ile Val Pro Val Cys Ser	
50 55 60	
TAT GAA GAG AGG GAG AAG CCC AAC TGT TTG AAT TTG CAG GAC TCC TGC	238
Tyr Glu Glu Arg Glu Lys Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys	
65 70 75	

AAG ACG AAT TAC ATC TGC AGA TCT CGC CTT GCG GAT TTT TTT ACC AAC	286
Lys Thr Asn Tyr Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn	
80 85 90 95	
TGC CAG CCA GAG TCA AGG TCT GTC AGC AGC TGT CTA AAG GAA AAC TAC	334
Cys Gln Pro Glu Ser Arg Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr	
100 105 110	
GCT GAC TGC CTC CTC GCC TAC TCG GGG CTT ATT GGC ACA GTC ATG ACC	382
Ala Asp Cys Leu Leu Ala Tyr Ser Gly Leu Ile Gly Thr Val Met Thr	
115 120 125	
CCC AAC TAC ATA GAC TCC AGT AGC CTC AGT GTG GCC CCA TGG TGT GAC	430
Pro Asn Tyr Ile Asp Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp	
130 135 140	
TGC AGC AAC AGT GGG AAC GAC CTA GAA GAG TGC TTG AAA TTT TTG AAT	478
Cys Ser Asn Ser Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn	
145 150 155	
TTC TTC AAG GAC AAT ACA TGT CTT AAA AAT GCA ATT CAA GCC TTT GGC	526
Phe Phe Lys Asp Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly	
160 165 170 175	
AAT GGC TCC GAT GTG ACC GTG TGG CAG CCA GCC TTC CCA GTA CAG ACC	574
Asn Gly Ser Asp Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr	
180 185 190	
ACC ACT GCC GCT ACC ACC ACT GCC CTC CGG GTT AAG AAC AAG CCC CTG	622
Thr Thr Ala Ala Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu	
195 200 205	
GGG CCA GCA GGG TCT GAG AAT GAA ATT CCC ACT CAT GTT TTG CCA CCG	670
Gly Pro Ala Gly Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro	
210 215 220	
TGT GCA AAT TTA CAG GCA CAG AAG CTG AA	699
Cys Ala Asn Leu Gln Ala Gln Lys Leu	
225 230	

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ser Ala Tyr Ile Thr Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys	
1 5 10 15	
Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val	
20 25 30	
Pro Ala Lys His Ser Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile	
35 40 45	
Ala Cys Thr Glu Arg Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr	
50 55 60	

Glu Glu Arg Glu Lys Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys
 65 70 75 80
 Thr Asn Tyr Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys
 85 90 95
 Gln Pro Glu Ser Arg Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala
 100 105 110
 Asp Cys Leu Leu Ala Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro
 115 120 125
 Asn Tyr Ile Asp Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys
 130 135 140
 Ser Asn Ser Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe
 145 150 155 160
 Phe Lys Asp Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn
 165 170 175
 Gly Ser Asp Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr
 180 185 190
 Thr Ala Ala Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly
 195 200 205
 Pro Ala Gly Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys
 210 215 220
 Ala Asn Leu Gln Ala Gln Lys Leu
 225 230

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..886

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..2157
- (D) OTHER INFORMATION: /note= "1 to 2157 is 814 to 2971 of Figure 5 29brc"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

G TCG GCG TAC ATC ACC CCG TGC ACC ACC AGC GTG TCC AAT GAT GTC	46
Ser Ala Tyr Ile Thr Pro Cys Thr Thr Ser Val Ser Asn Asp Val	
1 5 10 15	
TGC AAC CGC CGC AAG TGC CAC AAG GCC CTC CGG CAG TTC TTT GAC AAG	94
Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Lys	
20 25 30	

GTC	CCG	GCC	AAG	CAC	AGC	TAC	GGA	ATG	CTC	TTC	TGC	TCC	TGC	CGG	GAC	142
Val	Pro	Ala	Lys	His	Ser	Tyr	Gly	Met	Leu	Phe	Cys	Ser	Cys	Arg	Asp	
			35					40					45			
ATC	GCC	TGC	ACA	GAG	CGG	AGG	CGA	CAG	ACC	ATC	GTG	CCT	GTG	TGC	TCC	190
Ile	Ala	Cys	Thr	Glu	Arg	Arg	Arg	Gln	Thr	Ile	Val	Pro	Val	Cys	Ser	
		50					55					60				
TAT	GAA	GAG	AGG	GAG	AAG	CCC	AAC	TGT	TTG	AAT	TTG	CAG	GAC	TCC	TGC	238
Tyr	Glu	Glu	Arg	Glu	Lys	Pro	Asn	Cys	Leu	Asn	Leu	Gln	Asp	Ser	Cys	
	65					70					75					
AAG	ACG	AAT	TAC	ATC	TGC	AGA	TCT	CGC	CTT	GCG	GAT	TTT	TTT	ACC	AAC	286
Lys	Thr	Asn	Tyr	Ile	Cys	Arg	Ser	Arg	Leu	Ala	Asp	Phe	Phe	Thr	Asn	
	80				85					90					95	
TGC	CAG	CCA	GAG	TCA	AGG	TCT	GTC	AGC	AGC	TGT	CTA	AAG	GAA	AAC	TAC	334
Cys	Gln	Pro	Glu	Ser	Arg	Ser	Val	Ser	Ser	Cys	Leu	Lys	Glu	Asn	Tyr	
				100					105					110		
GCT	GAC	TGC	CTC	CTC	GCC	TAC	TCG	GGG	CTT	ATT	GGC	ACA	GTC	ATG	ACC	382
Ala	Asp	Cys	Leu	Leu	Ala	Tyr	Ser	Gly	Leu	Ile	Gly	Thr	Val	Met	Thr	
			115					120					125			
CCC	AAC	TAC	ATA	GAC	TCC	AGT	AGC	CTC	AGT	GTG	GCC	CCA	TGG	TGT	GAC	430
Pro	Asn	Tyr	Ile	Asp	Ser	Ser	Ser	Leu	Ser	Val	Ala	Pro	Trp	Cys	Asp	
		130					135					140				
TGC	AGC	AAC	AGT	GGG	AAC	GAC	CTA	GAA	GAG	TGC	TTG	AAA	TTT	TTG	AAT	478
Cys	Ser	Asn	Ser	Gly	Asn	Asp	Leu	Glu	Glu	Cys	Leu	Lys	Phe	Leu	Asn	
	145					150					155					
TTC	TTC	AAG	GAC	AAT	ACA	TGT	CTT	AAA	AAT	GCA	ATT	CAA	GCC	TTT	GGC	526
Phe	Phe	Lys	Asp	Asn	Thr	Cys	Leu	Lys	Asn	Ala	Ile	Gln	Ala	Phe	Gly	
	160				165					170					175	
AAT	GGC	TCC	GAT	GTG	ACC	GTG	TGG	CAG	CCA	GCC	TTC	CCA	GTA	CAG	ACC	574
Asn	Gly	Ser	Asp	Val	Thr	Val	Trp	Gln	Pro	Ala	Phe	Pro	Val	Gln	Thr	
				180					185					190		
ACC	ACT	GCC	GCT	ACC	ACC	ACT	GCC	CTC	CGG	GTT	AAG	AAC	AAG	CCC	CTG	622
Thr	Thr	Ala	Ala	Thr	Thr	Thr	Ala	Leu	Arg	Val	Lys	Asn	Lys	Pro	Leu	
			195					200					205			
GGG	CCA	GCA	GGG	TCT	GAG	AAT	GAA	ATT	CCC	ACT	CAT	GTT	TTG	CCA	CCG	670
Gly	Pro	Ala	Gly	Ser	Glu	Asn	Glu	Ile	Pro	Thr	His	Val	Leu	Pro	Pro	
		210					215					220				
TGT	GCA	AAT	TTA	CAG	GCA	CAG	AAG	CTG	AAA	TCC	AAT	GTG	TCG	GGC	AAT	718
Cys	Ala	Asn	Leu	Gln	Ala	Gln	Lys	Leu	Lys	Ser	Asn	Val	Ser	Gly	Asn	
		225				230					235					
ACA	CAC	CTC	TGT	ATT	TCC	AAT	GGT	AAT	TAT	GAA	AAA	GAA	GGT	CTC	GGT	766
Thr	His	Leu	Cys	Ile	Ser	Asn	Gly	Asn	Tyr	Glu	Lys	Glu	Gly	Leu	Gly	
		240			245					250					255	
GCT	TCC	AGC	CAC	ATA	ACC	ACA	AAA	TCA	ATG	GCT	GCT	CCT	CCA	AGC	TGT	814
Ala	Ser	Ser	His	Ile	Thr	Thr	Lys	Ser	Met	Ala	Ala	Pro	Pro	Ser	Cys	
				260					265					270		
GGT	CTG	AGC	CCA	CTG	CTG	GTC	CTG	GTG	GTA	ACC	GCT	CTG	TCC	ACC	CTA	862
Gly	Leu	Ser	Pro	Leu	Leu	Val	Leu	Val	Val	Thr	Ala	Leu	Ser	Thr	Leu	
			275					280					285			

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TTA TCT TTA ACA GAA ACA TCA TAG CTGCATTAAA AAAATACAAT ATGGACATGT      916
Leu Ser Leu Thr Glu Thr Ser *
      290                295

AAAAAGACAA AAACCAAGTT ATCTGTTTCC TGTTCTCTTG TATAGCTGAA ATTCCAGTTT      976
AGGAGCTCAG TTGAGAAACA GTTCCATTCA ACTGGAACAT TTTTTTTTTT CCTTTTAAGA      1036
AAGCTTCTTG TGATCCTTCG GGGCTTCTGT GAAAAACCTG ATGCAGTGCT CCATCCAAAC      1096
TCAGAAGGCT TTGGGATATG CTGTATTTTA AAGGGACAGT TTGTAAGTTG GGCTGTAAAG      1156
CAAAGTGGGG CTGTGTTTTC GATGATGATG ATCATCATGA TCATGATNNN NNNNNNNNNN      1216
NNNNNNNNNN NNNNNNNNNN NNNNNNGATT TTAACAGTTT TACTTCTGGC CTTTCCTAGC      1276
TAGAGAAGGA GTTAATATTT CTAAGGTAAC TCCCATATCT CCTTTAATGA CATTGATTTT      1336
TAATGATATA AATTTACAGC TACATTGATG CCAAGCTTTT TTGCCACAAA GAAGATTCTT      1396
ACCAAGAGTG GGCTTTGTGG AAACAGCTGG TACTGATGTT CACCTTTATA TATGTACTAG      1456
CATTTTCCAC GCTGATGTTT ATGTACTGTA AACAGTTCTG CACTCTTGTA CAAAAGAAAA      1516
AACACCTGTC ACATCCAAAT ATAGTATCTG TCTTTTCGTC AAAATAGAGA GTGGGGAATG      1576
AGTGTGCCGA TTCAATACCT CAATCCCTGA ACGACACTCT CCTAATCCTA AGCCTTACCT      1636
GAGTGAGAAG CCCTTTACCT AACAAAAGTC CAATATAGCT GAAATGTCGC TCTAATACTC      1696
TTTACACATA TGAGGTTATA TGTAGAAAAA AATTTTACTA CTAAATGATT TCAACTATTG      1756
GCTTTCTATA TTTTGAAAGT AATGATATTG TCTCATTTTT TTAGTGATGG TTTAATACAA      1816
AATACACAGA GCTTGTTTCC CCTCATAAGT AGTGTTCTGCT CTGATATGAA CTTACACAAAT      1876
ACAGCTCATC AAAAGCAGAC TCTGAGAAGC CTCGTGCTGT AGCAGAAAGT TCTGCATCAT      1936
GTGACTGTGG ACAGGCAGGA GGAAACAGAA CAGACAAGCA TTGTCTTTTG TCATTGCTCG      1996
AAGTGCAAGC GTGCATACCT GTGGAGGGAA CTGGTGGCTG CTTGTAAATG TTCTGCAGCA      2056
TCTCTTGACA CACTTGTCAT GACACAATCC AGTACCTTGG TTTTCAGGTT ATCTGACAAA      2116
GGCAGCTTTG ATTGGGACAT GGAGGCATGG GCAGGCCGGA A                        2157

```

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 295 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

Ser Ala Tyr Ile Thr Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys
 1           5           10           15

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Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val
      20           25           30

```

Pro Ala Lys His Ser Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile
 35 40 45
 Ala Cys Thr Glu Arg Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr
 50 55 60
 Glu Glu Arg Glu Lys Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys
 65 70 75 80
 Thr Asn Tyr Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys
 85 90 95
 Gln Pro Glu Ser Arg Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala
 100 105 110
 Asp Cys Leu Leu Ala Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro
 115 120 125
 Asn Tyr Ile Asp Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys
 130 135 140
 Ser Asn Ser Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe
 145 150 155 160
 Phe Lys Asp Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn
 165 170 175
 Gly Ser Asp Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr
 180 185 190
 Thr Ala Ala Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly
 195 200 205
 Pro Ala Gly Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys
 210 215 220
 Ala Asn Leu Gln Ala Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr
 225 230 235 240
 His Leu Cys Ile Ser Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala
 245 250 255
 Ser Ser His Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly
 260 265 270
 Leu Ser Pro Leu Leu Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu
 275 280 285
 Ser Leu Thr Glu Thr Ser *
 290 295

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 659 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 2..658

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1..659

(D) OTHER INFORMATION: /note= "1 to 659 is 1033 to 1691 of
Figure 5 Hsgr-21ar"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

G AAT TTG CAG GAC TCC TGC AAG ACG AAT TAC ATC TGC AGA TCT CGC	46
Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys Arg Ser Arg	
1 5 10 15	
CTT GCG GAT TTT TTT ACC AAC TGC CAG CCA GAG TCA AGG TCT GTC AGC	94
Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg Ser Val Ser	
20 25 30	
AGC TGT CTA AAG GAA AAC TAC GCT GAC TGC CTC CTC GCC TAC TCG GGG	142
Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala Tyr Ser Gly	
35 40 45	
CTT ATT GGC ACA GTC ATG ACC CCC AAC TAC ATA GAC TCC AGT AGC CTC	190
Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser Ser Ser Leu	
50 55 60	
AGT GTG GCC CCA TGG TGT GAC TGC AGC AAC AGT GGG AAC GAC CTA GAA	238
Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn Asp Leu Glu	
65 70 75	
GAG TGC TTG AAA TTT TTG AAT TTC TTC AAG GAC AAT ACA TGT CTT AAA	286
Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr Cys Leu Lys	
80 85 90 95	
AAT GCA ATT CAA GCC TTT GGC AAT GGC TCC GAT GTG ACC GTG TGG CAG	334
Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln	
100 105 110	
CCA GCC TTC CCA GTA CAG ACC ACC ACT GCC ACT ACC ACC ACT GCC CTC	382
Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr Thr Ala Leu	
115 120 125	
CGG GTT AAG AAC AAG CCC CTG GGG CCA GCA GGG TCT GAG AAT GAA ATT	430
Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu Asn Glu Ile	
130 135 140	
CCC ACT CAT GTT TTG CCA CCG TGT GCA AAT TTA CAG GCA CAG AAG CTG	478
Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala Gln Lys Leu	
145 150 155	
AAA TCC AAT GTG TCG GGC AAT ACA CAC CTC TGT ATT TCC AAT GGT AAT	526
Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser Asn Gly Asn	
160 165 170 175	
TAT GAA AAA GAA GGT CTC GGT GCT TCC AGC CAC ATA ACC ACA AAA TCA	574
Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr Thr Lys Ser	
180 185 190	
ATG GCT GCT CCT CCA AGC TGT GGT CTG AGC CCA CTG CTG GTC CTG GTG	622
Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu Val Leu Val	
195 200 205	

GTA ACC GCT CTG TCC ACC CTA TTA TCT TTA ACA GAA A
 Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu
 210 215

659

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys Arg Ser Arg Leu
 1 5 10 15
 Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg Ser Val Ser Ser
 20 25 30
 Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala Tyr Ser Gly Leu
 35 40 45
 Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser Ser Ser Leu Ser
 50 55 60
 Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn Asp Leu Glu Glu
 65 70 75 80
 Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr Cys Leu Lys Asn
 85 90 95
 Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln Pro
 100 105 110
 Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr Thr Ala Leu Arg
 115 120 125
 Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu Asn Glu Ile Pro
 130 135 140
 Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala Gln Lys Leu Lys
 145 150 155 160
 Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser Asn Gly Asn Tyr
 165 170 175
 Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr Thr Lys Ser Met
 180 185 190
 Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu Val Leu Val Val
 195 200 205
 Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu
 210 215

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 3..629

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..630

(D) OTHER INFORMATION: /note= "1 to 630 is 1062 to 1691 of Figure 5 Hsgr-21br"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AC ATC TGC AGA TCT CGC CTT GCG GAT TTT TTT ACC AAC TGC CAG CCA	47
Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro	
1 5 10 15	
GAG TCA AGG TCT GTC AGC AGC TGT CTA AAG GAA AAC TAC GCT GAC TGC	95
Glu Ser Arg Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys	
20 25 30	
CTC CTC GCC TAC TCG GGG CTT ATT GGC ACA GTC ATG ACC CCC AAC TAC	143
Leu Leu Ala Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr	
35 40 45	
ATA GAC TCC AGT AGC CTC AGT GTG GCC CCA TGG TGT GAC TGC AGC AAC	191
Ile Asp Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn	
50 55 60	
AGT GGG AAC GAC CTA GAA GAG TGC TTG AAA TTT TTG AAT TTC TTC AAG	239
Ser Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys	
65 70 75	
GAC AAT ACA TGT CTT AAA AAT GCA ATT CAA GCC TTT GGC AAT GGC TCC	287
Asp Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser	
80 85 90 95	
GAT GTG ACC GTG TGG CAG CCA GCC TTC CCA GTA CAG ACC ACC ACT GCC	335
Asp Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala	
100 105 110	
ACT ACC ACC ACT GCC CTC CGG GTT AAG AAC AAG CCC CTG GGG CCA GCA	383
Thr Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala	
115 120 125	
GGG TCT GAG AAT GAA ATT CCC ACT CAT GTT TTG CCA CCG TGT GCA AAT	431
Gly Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn	
130 135 140	
TTA CAG GCA CAG AAG CTG AAA TCC AAT GTG TCG GGC AAT ACA CAC CTC	479
Leu Gln Ala Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu	
145 150 155	
TGT ATT TCC AAT GGT AAT TAT GAA AAA GAA GGT CTC GGT GCT TCC AGC	527
Cys Ile Ser Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser	
160 165 170 175	
CAC ATA ACC ACA AAA TCA ATG GCT GCT CCT CCA AGC TGT GGT CTG AGC	575
His Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser	

	180	185	190	
CCA CTG CTG GTC CTG GTG GTA ACC GCT CTG TCC ACC CTA TTA TCT TTA				623
Pro Leu Leu Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu				
	195	200	205	
ACA GAA A				630
Thr Glu				

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ile	Cys	Arg	Ser	Arg	Leu	Ala	Asp	Phe	Phe	Thr	Asn	Cys	Gln	Pro	Glu	
1					5				10					15		
Ser	Arg	Ser	Val	Ser	Ser	Cys	Leu	Lys	Glu	Asn	Tyr	Ala	Asp	Cys	Leu	
			20					25					30			
Leu	Ala	Tyr	Ser	Gly	Leu	Ile	Gly	Thr	Val	Met	Thr	Pro	Asn	Tyr	Ile	
		35				40						45				
Asp	Ser	Ser	Ser	Leu	Ser	Val	Ala	Pro	Trp	Cys	Asp	Cys	Ser	Asn	Ser	
	50					55				60						
Gly	Asn	Asp	Leu	Glu	Glu	Cys	Leu	Lys	Phe	Leu	Asn	Phe	Phe	Lys	Asp	
	65				70					75					80	
Asn	Thr	Cys	Leu	Lys	Asn	Ala	Ile	Gln	Ala	Phe	Gly	Asn	Gly	Ser	Asp	
			85					90						95		
Val	Thr	Val	Trp	Gln	Pro	Ala	Phe	Pro	Val	Gln	Thr	Thr	Thr	Ala	Thr	
			100					105						110		
Thr	Thr	Thr	Ala	Leu	Arg	Val	Lys	Asn	Lys	Pro	Leu	Gly	Pro	Ala	Gly	
			115				120					125				
Ser	Glu	Asn	Glu	Ile	Pro	Thr	His	Val	Leu	Pro	Pro	Cys	Ala	Asn	Leu	
	130					135				140						
Gln	Ala	Gln	Lys	Leu	Lys	Ser	Asn	Val	Ser	Gly	Asn	Thr	His	Leu	Cys	
	145				150					155					160	
Ile	Ser	Asn	Gly	Asn	Tyr	Glu	Lys	Glu	Gly	Leu	Gly	Ala	Ser	Ser	His	
			165					170						175		
Ile	Thr	Thr	Lys	Ser	Met	Ala	Ala	Pro	Pro	Ser	Cys	Gly	Leu	Ser	Pro	
			180					185					190			
Leu	Leu	Val	Leu	Val	Val	Thr	Ala	Leu	Ser	Thr	Leu	Leu	Ser	Leu	Thr	
		195					200				205					
Glu																

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1075 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..445

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..1075

(D) OTHER INFORMATION: /note= "1 to 1075 is 1255 to 2330
of Figure 5 Hsgr-2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

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T GGG AAC GAC CTA GAA GAG TGC TTG AAA TTT TTG AAT TTC TTC AAG      46
  Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys
    1             5             10             15

GAC AAT ACA TGT CTT AAA AAT GCA ATT CAA GCC TTT GGC AAT GGC TCC      94
Asp Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser
          20             25             30

GAT GTG ACC GTG TGG CAG CCA GCC TTC CCA GTA CAG ACC ACC ACT GCC     142
Asp Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala
          35             40             45

ACT ACC ACC ACT GCC CTC CGG GTT AAG AAC AAG CCC CTG GGG CCA GCA     190
Thr Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala
          50             55             60

GGG TCT GAG AAT GAA ATT CCC ACT CAT GTT TTG CCA CCG TGT GCA AAT     238
Gly Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn
          65             70             75

TTA CAG GCA CAG AAG CTG AAA TCC AAT GTG TCG GGC AAT ACA CAC CTC     286
Leu Gln Ala Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu
          80             85             90             95

TGT ATT TCC AAT GGT AAT TAT GAA AAA GAA GGT CTC GGT GCT TCC AGC     334
Cys Ile Ser Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser
          100            105            110

CAC ATA ACC ACA AAA TCA ATG GCT GCT CCT CCA AGC TGT GGT CTG AGC     382
His Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser
          115            120            125

CCA CTG CTG GTC CTG GTG GTA ACC GCT CTG TCC ACC CTA TTA TCT TTA     430
Pro Leu Leu Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu
          130            135            140

ACA GAA ACA TCA TAG CTGCATTAAA AAAATACAAT ATGGACATGT AAAAAGACAA     485
Thr Glu Thr Ser *
          145

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AAACCAAGTT ATCTGTTTCC TGTTCTCTTG TATAGCTGAA ATTCCAGTTT AGGAGCTCAG      545
TTGAGAAACA GTTCCATTCA ACTGGAACAT TTTTTTTTTT CCTTTTAAGA AAGCTTCTTG      605
TGATCCTTCG GGGCTTCTGT GAAAAACCTG ATGCAGTGCT CCATCCAAAC TCAGAAGGCT      665
TTGGGATATG CTGTATTTTA AAGGGACAGT TTGTAAC TTG GGTGTAAAG CAAACTGGGG      725
CTGTGTTTTT GATGATGATG ATCATCATGA TCATGATNNN NNNNNNNNNN NNNNNNNNNN      785
NNNNNNNNNN NNNNNNGATT TTAACAGTTT TACTTCTGGC CTTTCCTAGC TAGAGAAGGA      845
GTTAATATTT CTAAGGTAAC TCCCATATCT CCTTTAATGA CATTGATTTC TAATGATATA      905
AATTTAGCC TACATTGATG CCAAGCTTTT TTGCCACAAA GAAGATTCTT ACCAAGAGTG      965
GGCTTTGTGG AACAGCTGG TACTGATGTT CACCTTTATA TATGTACTAG CATTTTCCAC     1025
GCTGATGTTT ATGTACTGTA AACAGTTCTG CACTCTTGTA CAAAAGAAAA     1075

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(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```

Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp
 1             5             10             15
Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp
      20             25             30
Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr
      35             40             45
Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly
      50             55             60
Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu
      65             70             75             80
Gln Ala Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys
      85             90             95
Ile Ser Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His
      100            105            110
Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro
      115            120            125
Leu Leu Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr
      130            135            140
Glu Thr Ser *
145

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(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1059 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 3..428

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..1059
 (D) OTHER INFORMATION: /note= "1 to 1059 is 1272 to 2330
 of Figure 5 Hsgr-9"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AG TGC TTG AAA TTT TTG AAT TTC TTC AAG GAC AAT ACA TGT CTT AAA	47
Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr Cys Leu Lys	
1 5 10 15	
AAT GCA ATT CAA GCC TTT GGC AAT GGC TCC GAT GTG ACC GTG TGG CAG	95
Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln	
20 25 30	
CCA GCC TTC CCA GTA CAG ACC ACC ACT GCC ACT ACC ACC ACT GCC CTC	143
Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr Thr Ala Leu	
35 40 45	
CGG GTT AAG AAC AAG CCC CTG GGG CCA GCA GGG TCT GAG AAT GAA ATT	191
Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu Asn Glu Ile	
50 55 60	
CCC ACT CAT GTT TTG CCA CCG TGT GCA AAT TTA CAG GCA CAG AAG CTG	239
Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala Gln Lys Leu	
65 70 75	
AAA TCC AAT GTG TCG GGC AAT ACA CAC CTC TGT ATT TCC AAT GGT AAT	287
Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser Asn Gly Asn	
80 85 90 95	
TAT GAA AAA GAA GGT CTC GGT GCT TCC AGC CAC ATA ACC ACA AAA TCA	335
Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr Thr Lys Ser	
100 105 110	
ATG GCT GCT CCT CCA AGC TGT GGT CTG AGC CCA CTG CTG GTC CTG GTG	383
Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu Val Leu Val	
115 120 125	
GTA ACC GCT CTG TCC ACC CTA TTA TCT TTA ACA GAA ACA TCA TAG	428
Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu Thr Ser *	
130 135 140	
CTGCATTAAA AAAATACAAT ATGGACATGT AAAAAGACAA AAACCAAGTT ATCTGTTTCC	488
TGTTCTCTTG TATAGCTGAA ATTCCAGTTT AGGAGCTCAG TTGAGAAACA GTTCCATTCA	548
ACTGGAACAT TTTTTTTTTT TCCTTTTAAG AAAGCTTCTT GTGATCCTTT GGGGCTTCTG	608

TGAAAAACCT GATGCAGTGC TCCATCCAAA CTCAGAAGGC TTTGGGATAT GCTGTATTTT 668
 AAAGGGACAG TTTGTAACCT GGGCTGTAAA GCAAAGTGGG GCTGTGTTTT CGATGATGAT 728
 GATGATCATG ATGATGATCA TCATGATCAT GATGATGATC ATCATGATCA TGATGATGAT 788
 TTAAACAGTT TTAATTCTGG CCTTTCCTAG CTAGAGAAGG AGTTAATATT TCTAAGGTAA 848
 CTCCCATATC TCCTTTAATG ACATTGATTT CTAATGATAT AAATTTTCAGC CTACATTGAT 908
 GCCAAGCTTT TTTGCCACAA AGAAGATTCT TACCAAGAGT GGGCTTTGTG GAAACAGCTG 968
 GTACTGATGT TCACCTTTAT ATATGTACTA GCATTTTCCA CGCTGATGTT TATGTACTGT 1028
 AAACAGTTCT GCACTCTTGT ACAAAGAAA A 1059

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr Cys Leu Lys Asn
 1 5 10 15
 Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln Pro
 20 25 30
 Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr Thr Ala Leu Arg
 35 40 45
 Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu Asn Glu Ile Pro
 50 55 60
 Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala Gln Lys Leu Lys
 65 70 75 80
 Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser Asn Gly Asn Tyr
 85 90 95
 Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr Thr Lys Ser Met
 100 105 110
 Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu Val Leu Val Val
 115 120 125
 Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu Thr Ser *
 130 135 140

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Gln	Ser	Cys	Ser	Thr	Lys	Tyr	Arg	Thr	Leu
1				5					10

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Cys	Lys	Arg	Gly	Met	Lys	Lys	Glu	Lys	Asn
1				5					10

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Leu	Leu	Glu	Asp	Ser	Pro	Tyr	Glu	Pro	Val
1				5					10

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Cys	Ser	Tyr	Glu	Glu	Arg	Glu	Arg	Pro	Asn
1				5					10

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Pro	Ala	Pro	Pro	Val	Gln	Thr	Thr	Thr	Ala	Thr	Thr	Thr	Thr
1				5					10				

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CTGTTTGAAT TTGCAGGACT C

21

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CTCCTCTCTA AGCTTCTAAC CACAGCTTGG AGGAGC

36

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTCCTCTCTA AGCTTCTATG GGCTCAGACC ACAGCTT

37

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CTCCTCTCTA AGCTTCTACT TGTCATCGTC GTCCTTGTAG TCACCACAGC TTGGAGGAGC

60

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CTCCTCTCTA AGCTTCTACT TGTCATCGTC GTCCTTGTAG TCTGGCTCAG ACCACAGCTT

60

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1587..2978

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CATGAAGAAA CCTCAGTAAG TCTCAGACTT GGCCCAAAGG AGCCCAACTA GTTACTCCCT

60

GGTCTGTTAC AGAGGATCTG GCTATTACAC TCAACAGCAA AAATTCAATT CAATCCCGCT

120

AAAGATATAA GAATCACTAG GAAKAATAAG CCAGAACTCA AGACAGAAAT AGCATTAAGT

180

AGTTCCTTCA GTACAGTGAG CAGAAGCTGG CCACTCTACG ACTCTAWAAG ACTCAGAAAA	240
GCTTACTAGG GACCWCTGGG CATWCCGGTG TCCTATGTGG GGATTTCGTA ACGTCTTTGA	300
GTCAGAAGCT GCCCTCAAAA TAGTTTCTTC TCAAAACGGT TTCAGGCTTT GTTAGAAAGG	360
GAAGACTTCA CTGCCACTTT ACCCAGATCA TCTACCCCAT CCTTGGAATG AATGGGGAAG	420
CTTCAGCCAC CCTACCAGGC TCCTAAAATC ACCAACTTGA GAGAAAAACT ATAACGTTGC	480
TCTACCAGTA CTTCAGGAGG TTAAAGAAAG TCACAGAAGA AAAGAACTCT GGGGAAAACA	540
GTCAAATTCG GCTATTAAGA CATTAGTTAC AGGCCCTGT ACCTCTCCTC TAGAAACCCT	600
GGGAGTACAC CCGCAGAGGA GAGAGAGCCC AAGCCACCAA GCAAAGTCAA CCAATCTGGC	660
AAAGGGGCGT CCCACTGCGG CTTTCAGTCC AAGAAGTGGG TCCTGCTGGT TCGCAGTCTC	720
TCTTCTATCT CCTCACTTCC TATTTACCCT TTGAAGTGGG TACTGAATAG CCCGTTCCCA	780
AGCAGAGGCC CTTTGTATAC GGGGTGCTAC AGTCGCCTGG TGGAAACACC TTGGCAGAGT	840
TGTTTGGTGC CAGGATGGGC CACTGAAGGC ATCTGCTGTG GACACACACA CACACACACA	900
CACACACACA CACACACACA GAGAGAGGAG AGAGAAAGAC ACACGCACGC AGAGACACAC	960
GGTCACTGGA ATTCCATTAG AAAAAAGTGA GCCGAGCAAG GGTTAGCGGG AGAAGATTTT	1020
TTGAATCTT GTCTTCGTCT TGGTGCGAAA GAAGCGACTC CAGTCTCTCG TCCTCGAAGC	1080
TCCGACTGGA TTGTCTTGG GCGCTGACAC CCGTCTGTGG ATTTCTTTTC TATTTGCATT	1140
TTATTCGGAC CCCCTCCCTC GCCGCTTCCT TCCAGCCCTT CACTCGCAA TCGCCTCTCT	1200
CCCCACCTCC CCAGGCCCTT CCTGGGAAGC GCAGGGGAAT TGGACCCGCG GGGACTCACG	1260
CCTTCCCGGA CGATTGGAGG GGAGGGCTGA CCCCAGGACT GGGCTGTTGG CTTAGAAAGC	1320
CGATACACAG ATACGCGTAT ATTTGATTGT AGCGGGCAAG GGGGGCGTCG AGAGGCAGCA	1380
GCCCATCGCC CGCCTCTCAC CCCACCCCTT CCAGCCAGAG GCGAGAATCG CAGGACTCGG	1440
GATCTTCATC GGGTGGACTA GCTGGGATCT CCGCATTGGA TTTGGGGCTG ATTACCACTG	1500
CTTGGCTATT ATTATTGTTG TTGTTACTAC TATTATTTTT TTTTACCCAA GGGAGAAAGA	1560
CAAAAAACG GTGGGATTTA TTAAAC ATG ATC TTG GCA AAC GTC TTC TGC CTC	1613
Met Ile Leu Ala Asn Val Phe Cys Leu	
1 5	
TTC TTC TTT CTA GAC GAC ACC CTC CGC TCT TTG GCC AGC CCT TCC TCC	1661
Phe Phe Phe Leu Asp Asp Thr Leu Arg Ser Leu Ala Ser Pro Ser Ser	
10 15 20 25	
CTG CAG GGC CCC GAG CTC CAC GGC TGG CGC CCC CCA GTG GAC TGT GTC	1709
Leu Gln Gly Pro Glu Leu His Gly Trp Arg Pro Pro Val Asp Cys Val	
30 35 40	
CGG GCC AAT GAG CTG TGT GCC GCC GAA TCC AAC TGC AGC TCT CGC TAC	1757
Arg Ala Asn Glu Leu Cys Ala Ala Glu Ser Asn Cys Ser Ser Arg Tyr	
45 50 55	
CGC ACT CTG CGG CAG TGC CTG GCA GGC CGC GAC CGC AAC ACC ATG CTG	1805
Arg Thr Leu Arg Gln Cys Leu Ala Gly Arg Asp Arg Asn Thr Met Leu	

60	65	70	
GCC AAC AAG GAG TGC CAG GCG GCC TTG GAG GTC TTG CAG GAG AGC CCG Ala Asn Lys Glu Cys Gln Ala Ala Leu Glu Val Leu Gln Glu Ser Pro 75 80 85			1853
CTG TAC GAC TGC CGC TGC AAG CGG GGC ATG AAG AAG GAG CTG CAG TGT Leu Tyr Asp Cys Arg Cys Lys Arg Gly Met Lys Lys Glu Leu Gln Cys 90 95 100 105			1901
CTG CAG ATC TAC TGG AGC ATC CAC CTG GGG CTG ACC GAG GGT GAG GAG Leu Gln Ile Tyr Trp Ser Ile His Leu Gly Leu Thr Glu Gly Glu Glu 110 115 120			1949
TTC TAC GAA GCC TCC CCC TAT GAG CCG GTG ACC TCC CGC CTC TCG GAC Phe Tyr Glu Ala Ser Pro Tyr Glu Pro Val Thr Ser Arg Leu Ser Asp 125 130 135			1997
ATC TTC AGG CTT GCT TCA ATC TTC TCA GGG ACA GGG GCA GAC CCG GTG Ile Phe Arg Leu Ala Ser Ile Phe Ser Gly Thr Gly Ala Asp Pro Val 140 145 150			2045
GTC AGC GCC AAG AGC AAC CAT TGC CTG GAT GCT GCC AAG GCC TGC AAC Val Ser Ala Lys Ser Asn His Cys Leu Asp Ala Ala Lys Ala Cys Asn 155 160 165			2093
CTG AAT GAC AAC TGC AAG AAG CTG CGC TCC TCC TAC ATC TCC ATC TGC Leu Asn Asp Asn Cys Lys Lys Leu Arg Ser Ser Tyr Ile Ser Ile Cys 170 175 180 185			2141
AAC CGC GAG ATC TCG CCC ACC GAG CGC TGC AAC CGC CGC AAG TGC CAC Asn Arg Glu Ile Ser Pro Thr Glu Arg Cys Asn Arg Arg Lys Cys His 190 195 200			2189
AAG GCC CTG CGC CAG TTC TTC GAC CGG GTG CCC AGC GAG TAC ACC TAC Lys Ala Leu Arg Gln Phe Phe Asp Arg Val Pro Ser Glu Tyr Thr Tyr 205 210 215			2237
CGC ATG CTC TTC TGC TCC TGC CAA GAC CAG GCG TGC GCT GAG CGC CGC Arg Met Leu Phe Cys Ser Cys Gln Asp Gln Ala Cys Ala Glu Arg Arg 220 225 230			2285
CGG CAA ACC ATC CTG CCC AGC TGC TCC TAT GAG GAC AAG GAG AAG CCC Arg Gln Thr Ile Leu Pro Ser Cys Ser Tyr Glu Asp Lys Glu Lys Pro 235 240 245			2333
AAC TGC CTG GAC CTG CGT GGC GTG TGC CGG ACT GAC CAC CTG TGT CGG Asn Cys Leu Asp Leu Arg Gly Val Cys Arg Thr Asp His Leu Cys Arg 250 255 260 265			2381
TCC CGG CTG GCC GAC TTC CAT GCC AAT TGT CGA GCC TCC TAC CAG ACG Ser Arg Leu Ala Asp Phe His Ala Asn Cys Arg Ala Ser Tyr Gln Thr 270 275 280			2429
GTC ACC AGC TGC CCT GCG GAC AAT TAC CAG GCG TGT CTG GGC TCT TAT Val Thr Ser Cys Pro Ala Asp Asn Tyr Gln Ala Cys Leu Gly Ser Tyr 285 290 295			2477
GCT GGC ATG ATT GGG TTT GAC ATG ACA CCT AAC TAT GTG GAC TCC AGC Ala Gly Met Ile Gly Phe Asp Met Thr Pro Asn Tyr Val Asp Ser Ser 300 305 310			2525
CCC ACT GGC ATC GTG GTG TCC CCC TGG TGC AGC TGT CGT GGC AGC GGG Pro Thr Gly Ile Val Val Ser Pro Trp Cys Ser Cys Arg Gly Ser Gly			2573

315	320	325	
AAC ATG GAG GAG GAG TGT GAG AAG TTC CTC AGG GAC TTC ACC GAG AAC Asn Met Glu Glu Glu Cys Glu Lys Phe Leu Arg Asp Phe Thr Glu Asn 330 335 340 345	2621		
CCA TGC CTC CGG AAC GCC ATC CAG GCC TTT GGC AAC GGC ACG AAC GTG Pro Cys Leu Arg Asn Ala Ile Gln Ala Phe Gly Asn Gly Thr Asn Val 350 355 360	2669		
AAC GTG TCC CCA AAA GGC CCC TCG TTC CAG GCC ACC CAG GCC CCT CGG Asn Val Ser Pro Lys Gly Pro Ser Phe Gln Ala Thr Gln Ala Pro Arg 365 370 375	2717		
GTG GAG AAG ACG CCT TCT TTG CCA GAT GAC CTC AGT GAC AGT ACC AGC Val Glu Lys Thr Pro Ser Leu Pro Asp Asp Leu Ser Asp Ser Thr Ser 380 385 390	2765		
TTG GGG ACC AGT GTC ATC ACC ACC TGC ACG TCT GTC CAG GAG CAG GGG Leu Gly Thr Ser Val Ile Thr Cys Thr Ser Val Gln Glu Gln Gly 395 400 405	2813		
CTG AAG GCC AAC AAC TCC AAA GAG TTA AGC ATG TGC TTC ACA GAG CTC Leu Lys Ala Asn Asn Ser Lys Glu Leu Ser Met Cys Phe Thr Glu Leu 410 415 420 425	2861		
ACG ACA AAT ATC ATC CCA GGG AGT AAC AAG GTG ATC AAA CCT AAC TCA Thr Thr Asn Ile Ile Pro Gly Ser Asn Lys Val Ile Lys Pro Asn Ser 430 435 440	2909		
GGC CCC AGC AGA GCC AGA CCG TCG GCT GCC TTG ACC GTG CTG TCT GTC Gly Pro Ser Arg Ala Arg Pro Ser Ala Ala Leu Thr Val Leu Ser Val 445 450 455	2957		
CTG ATG CTG AAA CTG GCC TTG TAGGCTGTGG GAACCGAGTC AGAAGATTTT Leu Met Leu Lys Leu Ala Leu 460	3008		
TGAAAGCTAC GCAGACAAGA ACAGCCGCCT GACGAAATGG AAACACACAC AGACACACAC	3068		
ACACCTTGCA AAAAAAAT TGTTTTTCCC ACCTTGTCGC TGAACCTGTC TCCTCCCAGG	3128		
TTTCTTCTCT GGAGAAGTTT TTGTAAACCA AACAGACAAG CAGGCAGGCA GCCTGAGAGC	3188		
TGGCCCAGGG GTCCCCTGGC AGGGGAAACT CTGGTGCCGG GGAGGGCACG AGGCTCTAGA	3248		
AATGCCCTTC ACTTCTCCT GGTGTTTTTC TCTCTGGACC CTTCTGAAGC AGAGACCGGA	3308		
CAAGAGCCTG CAGCGGAAGG GACTCTGGGC TGTGCCTGAG GCTGGCTGGG GGCAGGACAA	3368		
CACAGCTGCT TCCCCAGGCT GCCCACTCTG GGGACCCGCT GGGGGCTGGC AGAGGGCATC	3428		
GGTCAGCGGG GCAGCGGGGC TGGCCATGAG GGTCCACCTT CAGCCCTTTG GCTTCAAGGA	3488		
TGGAGATGGT TTTGCCCTCC CTCTCTGCCC TCGGGTGGGG CTGGTGGGTC TGCAGCTGGT	3548		
GTGGGAACCT CCCACGGAT GGCGGTGGAG GGGGTTTCGA CCGTGCTGGG CTCCCCCTGA	3608		
CTGTAGCACG GAGTGTGGG GCTGGGGGCC AGCTCCAGGA GGGCTTGAGA GCTCAGCCTG	3668		
CCTGGGAGAG CCCTTGTTGGC GAGGCATTAA AACTTGGGCA CCAGCTTCTT TCTCGGTGGC	3728		
AGAAATTTTG AAGTCAGAGA GAAACGGTCC TTTGTTGGCT TCTTTGCTTT CTCGTGGGTC	3788		

CTTTGGCAGG CCTCCCTTTG GGGAGAGGGA GGGGAGAGAC CACAGCCGGG TGTGTGTCTG 3848
 CAGCACCGTG GGCCCTCAAG CTTTCCTGCT GTCTTCTCCC TCCTCCTCCT TTCCCCTTTC 3908
 TCTTTCTCTCA TTTCCTAGAC GTACGTCAAC TGTATGTACA TACCGGGGCT CCTCTCTCAA 3968
 CATATATGTA TATACACATC CATATACATA TATTGTGTGG TTTCCCCTTT CTTTCCTTTT 4028
 TTTAAGCAAC AAAACTATGG AAATAATACC CCAACAGATG AGCGAAAATG TATTATTGTA 4088
 AAGTTTATTT TTTTAAATAC TGTGTCTAT AATGGGGAAA AAGGACATTG GCCCCGCAGT 4148
 GCCCTGCCCC AGTCAGCCTG GCTGGGCTCT GGTGGGGGCT CCTGATCCGC ATCCAAGCTT 4208
 AACCAAGGCT CCAATAAACG TGCG 4232

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Ile Leu Ala Asn Val Phe Cys Leu Phe Phe Phe Leu Asp Asp Thr
 1 5 10 15
 Leu Arg Ser Leu Ala Ser Pro Ser Ser Leu Gln Gly Pro Glu Leu His
 20 25 30
 Gly Trp Arg Pro Pro Val Asp Cys Val Arg Ala Asn Glu Leu Cys Ala
 35 40 45
 Ala Glu Ser Asn Cys Ser Ser Arg Tyr Arg Thr Leu Arg Gln Cys Leu
 50 55 60
 Ala Gly Arg Asp Arg Asn Thr Met Leu Ala Asn Lys Glu Cys Gln Ala
 65 70 75 80
 Ala Leu Glu Val Leu Gln Glu Ser Pro Leu Tyr Asp Cys Arg Cys Lys
 85 90 95
 Arg Gly Met Lys Lys Glu Leu Gln Cys Leu Gln Ile Tyr Trp Ser Ile
 100 105 110
 His Leu Gly Leu Thr Glu Gly Glu Glu Phe Tyr Glu Ala Ser Pro Tyr
 115 120 125
 Glu Pro Val Thr Ser Arg Leu Ser Asp Ile Phe Arg Leu Ala Ser Ile
 130 135 140
 Phe Ser Gly Thr Gly Ala Asp Pro Val Val Ser Ala Lys Ser Asn His
 145 150 155 160
 Cys Leu Asp Ala Ala Lys Ala Cys Asn Leu Asn Asp Asn Cys Lys Lys
 165 170 175
 Leu Arg Ser Ser Tyr Ile Ser Ile Cys Asn Arg Glu Ile Ser Pro Thr
 180 185 190

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1991 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 203..1402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CAAGTCAAAG GTTTAATCAT GATCCAAGAG CCCAGAGAGA CTTTAGGACA ATAATAGGAA	60
TAAAGCAAGG CCCACAGGCT CCAGCTCCTG ATGCCAGAT GTTCGGCAGG ATCCGGGGAC	120
AGGGCAGTGC AGGCAGTAGT TTTCCATCCT CCATCCAGGG GAGGAGCGAG GGGAGCGCGG	180
AGCCCCGGCGC CTACAGCTCG CC ATG GTG CGC CCC CTG AAC CCG CGA CCG CTG	232
Met Val Arg Pro Leu Asn Pro Arg Pro Leu	
1 5 10	
CCG CCC GTA GTC CTG ATG TTG CTG CTG CTG CCG CCG TCG CCG CTG	280
Pro Pro Val Val Leu Met Leu Leu Leu Leu Leu Pro Pro Ser Pro Leu	
15 20 25	
CCT CTC GCA GCC GGA GAC CCC CTT CCC ACA GAA AGC CGA CTC ATG AAC	328
Pro Leu Ala Ala Gly Asp Pro Leu Pro Thr Glu Ser Arg Leu Met Asn	
30 35 40	
AGC TGT CTC CAG GCC AGG AGG AAG TGC CAG GCT GAT CCC ACC TGC AGT	376
Ser Cys Leu Gln Ala Arg Arg Lys Cys Gln Ala Asp Pro Thr Cys Ser	
45 50 55	
GCT GCC TAC CAC CAC CTG GAT TCC TGC ACC TCT AGC ATA AGC ACC CCA	424
Ala Ala Tyr His His Leu Asp Ser Cys Thr Ser Ser Ile Ser Thr Pro	
60 65 70	
CTG CCC TCA GAG GAG CCT TCG GTC CCT GCT GAC TGC CTG GAG GCA GCA	472
Leu Pro Ser Glu Glu Pro Ser Val Pro Ala Asp Cys Leu Glu Ala Ala	
75 80 85 90	
CAG CAA CTC AGG AAC AGC TCT CTG ATA GGC TGC ATG TGC CAC CGG CGC	520
Gln Gln Leu Arg Asn Ser Ser Leu Ile Gly Cys Met Cys His Arg Arg	
95 100 105	
ATG AAG AAC CAG GTT GCC TGC TTG GAC ATC TAT TGG ACC GTT CAC CGT	568
Met Lys Asn Gln Val Ala Cys Leu Asp Ile Tyr Trp Thr Val His Arg	
110 115 120	
GCC CGC AGC CTT GGT AAC TAT GAG CTG GAT GTC TCC CCC TAT GAA GAC	616
Ala Arg Ser Leu Gly Asn Tyr Glu Leu Asp Val Ser Pro Tyr Glu Asp	
125 130 135	
ACA GTG ACC AGC AAA CCC TGG AAA ATG AAT CTC AGC AAA CTG AAC ATG	664
Thr Val Thr Ser Lys Pro Trp Lys Met Asn Leu Ser Lys Leu Asn Met	
140 145 150	
CTC AAA CCA GAC TCA GAC CTC TGC CTC AAG TTT GCC ATG CTG TGT ACT	712
Leu Lys Pro Asp Ser Asp Leu Cys Leu Lys Phe Ala Met Leu Cys Thr	
155 160 165 170	
CTC AAT GAC AAG TGT GAC CGG CTG CGC AAG GCC TAC GGG GAG GCG TGC	760
Leu Asn Asp Lys Cys Asp Arg Leu Arg Lys Ala Tyr Gly Glu Ala Cys	
175 180 185	
TCC GGG CCC CAC TGC CAG CGC CAC GTC TGC CTC AGG CAG CTG CTC ACT	808
Ser Gly Pro His Cys Gln Arg His Val Cys Leu Arg Gln Leu Leu Thr	
190 195 200	

TTC	TTC	GAG	AAG	GCC	GCC	GAG	CCC	CAC	GCG	CAG	GGC	CTG	CTA	CTG	TGC	856
Phe	Phe	Glu	Lys	Ala	Ala	Glu	Pro	His	Ala	Gln	Gly	Leu	Leu	Leu	Cys	
		205					210					215				
CCA	TGT	GCC	CCC	AAC	GAC	CGG	GGC	TGC	GGG	GAG	CGC	CGG	CGC	AAC	ACC	904
Pro	Cys	Ala	Pro	Asn	Asp	Arg	Gly	Cys	Gly	Glu	Arg	Arg	Arg	Asn	Thr	
		220				225					230					
ATC	GCC	CCC	AAC	TGC	GCG	CTG	CCG	CCT	GTG	GCC	CCC	AAC	TGC	CTG	GAG	952
Ile	Ala	Pro	Asn	Cys	Ala	Leu	Pro	Pro	Val	Ala	Pro	Asn	Cys	Leu	Glu	
		235			240					245					250	
CTG	CGG	CGC	CTC	TGC	TTC	TCC	GAC	CCG	CTT	TGC	AGA	TCA	CGC	CTG	GTG	1000
Leu	Arg	Arg	Leu	Cys	Phe	Ser	Asp	Pro	Leu	Cys	Arg	Ser	Arg	Leu	Val	
			255						260					265		
GAT	TTC	CAG	ACC	CAC	TGC	CAT	CCC	ATG	GAC	ATC	CTA	GGA	ACT	TGT	GCA	1048
Asp	Phe	Gln	Thr	His	Cys	His	Pro	Met	Asp	Ile	Leu	Gly	Thr	Cys	Ala	
			270					275					280			
ACA	GAG	CAG	TCC	AGA	TGT	CTA	CGA	GCA	TAC	CTG	GGG	CTG	ATT	GGG	ACT	1096
Thr	Glu	Gln	Ser	Arg	Cys	Leu	Arg	Ala	Tyr	Leu	Gly	Leu	Ile	Gly	Thr	
		285					290					295				
GCC	ATG	ACC	CCC	AAC	TTT	GCC	AGC	AAT	GTC	AAC	ACC	AGT	GTT	GCC	TTA	1144
Ala	Met	Thr	Pro	Asn	Phe	Ala	Ser	Asn	Val	Asn	Thr	Ser	Val	Ala	Leu	
		300				305					310					
AGC	TGC	ACC	TGC	CGA	GGC	AGT	GGC	AAC	CTG	CAG	GAG	GAG	TGT	GAA	ATG	1192
Ser	Cys	Thr	Cys	Arg	Gly	Ser	Gly	Asn	Leu	Gln	Glu	Glu	Cys	Glu	Met	
		315			320					325				330		
CTG	GAA	GGG	TTC	TTC	TCC	CAC	AAC	CCC	TGC	CTC	ACG	GAG	GCC	ATT	GCA	1240
Leu	Glu	Gly	Phe	Phe	Ser	His	Asn	Pro	Cys	Leu	Thr	Glu	Ala	Ile	Ala	
			335						340					345		
GCT	AAG	ATG	CGT	TTT	CAC	AGC	CAA	CTC	TTC	TCC	CAG	GAC	TGG	CCA	CAC	1288
Ala	Lys	Met	Arg	Phe	His	Ser	Gln	Leu	Phe	Ser	Gln	Asp	Trp	Pro	His	
			350					355					360			
CCT	ACC	TTT	GCT	GTG	ATG	GCA	CAC	CAG	AAT	GAA	AAC	CCT	GCT	GTG	AGG	1336
Pro	Thr	Phe	Ala	Val	Met	Ala	His	Gln	Asn	Glu	Asn	Pro	Ala	Val	Arg	
		365					370					375				
CCA	CAG	CCC	TGG	GTG	CCC	TCT	CTT	TTC	TCC	TGC	ACG	CTT	CCC	TTG	ATT	1384
Pro	Gln	Pro	Trp	Val	Pro	Ser	Leu	Phe	Ser	Cys	Thr	Leu	Pro	Leu	Ile	
		380				385					390					
CTG	CTC	CTG	AGC	CTA	TGG	TAGCTGGACT TCCCCAGGGC CCTCTTCCCC									1432	
Leu	Leu	Leu	Ser	Leu	Trp	400										
TCCACCACAC	CCAGGTGGAC	TTGCAGCCCA	CAAGGGGTGA	GGAAAGGACA	GCAGCAGGAA											1492
GGAGGTGCAG	TGCGCAGATG	AGGGCACAGG	AGAAGCTAAG	GGTTATGACC	TCCAGATCCT											1552
TACTGGTCCA	GTCCTCATTC	CCTCCACCCC	ATCTCCACTT	CTGATTCATG	CTGCCCTCC											1612
TTGGTGGCCA	CAATTTAGCC	ATGTCATCTG	GTGGTGACCA	GCTCCACCAA	GCCCCTTTGT											1672
GAGCCCTTCC	TCTTGACTAC	CAGGATCACC	AGAATCTAAT	AAGTTAGCCT	TTCTCTATTG											1732
CATTCCAGAT	TAGGGTTAGG	GTAGGGAGGA	CTGGGTGTTC	TGAGGCAGCC	TAGAAAGTCA											1792

TTCTCCTTTG TGAAGAAGGC TCCTGCCCCC TCGTCTCCTC CTCTGAGTGG AGGATGGAAA 1852
 ACTACTGCCT GCACTGCCCT GTCCCCGGAT CCTGCCGAAC ATCTGGGCAT CAGGAGCTGG 1912
 AGCCTGTGGG CCTTGCTTTA TTCCTATTAT TGTCCCTAAAG TCTCTCTGGG CTCTTGGATC 1972
 ATGATTAAAC CTTTGACTG 1991

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met Val Arg Pro Leu Asn Pro Arg Pro Leu Pro Pro Val Val Leu Met
 1 5 10 15
 Leu Leu Leu Leu Pro Pro Ser Pro Leu Pro Leu Ala Ala Gly Asp
 20 25 30
 Pro Leu Pro Thr Glu Ser Arg Leu Met Asn Ser Cys Leu Gln Ala Arg
 35 40 45
 Arg Lys Cys Gln Ala Asp Pro Thr Cys Ser Ala Ala Tyr His His Leu
 50 55 60
 Asp Ser Cys Thr Ser Ser Ile Ser Thr Pro Leu Pro Ser Glu Glu Pro
 65 70 75 80
 Ser Val Pro Ala Asp Cys Leu Glu Ala Ala Gln Gln Leu Arg Asn Ser
 85 90 95
 Ser Leu Ile Gly Cys Met Cys His Arg Arg Met Lys Asn Gln Val Ala
 100 105 110
 Cys Leu Asp Ile Tyr Trp Thr Val His Arg Ala Arg Ser Leu Gly Asn
 115 120 125
 Tyr Glu Leu Asp Val Ser Pro Tyr Glu Asp Thr Val Thr Ser Lys Pro
 130 135 140
 Trp Lys Met Asn Leu Ser Lys Leu Asn Met Leu Lys Pro Asp Ser Asp
 145 150 155 160
 Leu Cys Leu Lys Phe Ala Met Leu Cys Thr Leu Asn Asp Lys Cys Asp
 165 170 175
 Arg Leu Arg Lys Ala Tyr Gly Glu Ala Cys Ser Gly Pro His Cys Gln
 180 185 190
 Arg His Val Cys Leu Arg Gln Leu Leu Thr Phe Phe Glu Lys Ala Ala
 195 200 205
 Glu Pro His Ala Gln Gly Leu Leu Leu Cys Pro Cys Ala Pro Asn Asp
 210 215 220
 Arg Gly Cys Gly Glu Arg Arg Arg Asn Thr Ile Ala Pro Asn Cys Ala
 225 230 235 240

Leu Pro Pro Val Ala Pro Asn Cys Leu Glu Leu Arg Arg Leu Cys Phe
 245 250 255
 Ser Asp Pro Leu Cys Arg Ser Arg Leu Val Asp Phe Gln Thr His Cys
 260 265 270
 His Pro Met Asp Ile Leu Gly Thr Cys Ala Thr Glu Gln Ser Arg Cys
 275 280 285
 Leu Arg Ala Tyr Leu Gly Leu Ile Gly Thr Ala Met Thr Pro Asn Phe
 290 295 300
 Ala Ser Asn Val Asn Thr Ser Val Ala Leu Ser Cys Thr Cys Arg Gly
 305 310 315 320
 Ser Gly Asn Leu Gln Glu Glu Cys Glu Met Leu Glu Gly Phe Phe Ser
 325 330 335
 His Asn Pro Cys Leu Thr Glu Ala Ile Ala Ala Lys Met Arg Phe His
 340 345 350
 Ser Gln Leu Phe Ser Gln Asp Trp Pro His Pro Thr Phe Ala Val Met
 355 360 365
 Ala His Gln Asn Glu Asn Pro Ala Val Arg Pro Gln Pro Trp Val Pro
 370 375 380
 Ser Leu Phe Ser Cys Thr Leu Pro Leu Ile Leu Leu Leu Ser Leu Trp
 385 390 395 400

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 684..2063

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CGGCCCGCGT CGACCTTGAC CATGCAGACA CTTTTTCAGG CCTCTGTCTG GTGTGAAGTT	60
GGCAGATACA AGCAAGGCC GAAAGGGGTC TCAGCTTCTC TCTCCTGGGC CTCCTGGACT	120
GAGTTAGGCT TGCTTCTGGT TGTCTTCTAA AGGCACGGTG ATACAGAATG ATGAGACTAG	180
GCTGGAGGGG GCTTCTGCT TCTCTGTGTG TGACCTTGAG TTATCTCCCT TCGTTGGATC	240
CGAGCTTTCC TGGAATATGA TGTGGAATAT GAATATGAGT TCTGCCTAAG GTCCAGACAG	300
GCTCTGAGGG TTAAGTACT TTTGGAGCCT TCAAATCAAT ACCTTGGATG GAGTGGGGGT	360
TTGTCCAATG GGAGTTGAGG CAAGATCCCT TTGCATAAGC CTTGCCACAT CATGTTGAAG	420

CCATGCCATT CTGTCTGGAC TATTGGCATC TTACCTTTCC AGCAGTTTCA GTGAAGGCCT	480
TCCTGGATTT ATCATTTCTGT GTTCCACTGC CTAGGATTGT GCTCAAGAGG AAATGAATGT	540
GAACCATGGT TGTAGGGGAG TATGGCCAAC CAGGTTGGGT CTGTGTTGAC CTTGGTCTTG	600
GTGTTCTTTT GTGTAAAGTG GGTGAGAAGT TCCTTCAAAC CTTAGGCCTA CATTGGGGTC	660
AGAGACTGTG GTGGCCCTCA TTC ATG CTT GTC TTC CCT TCC CAC TAC CCA	710
Met Leu Val Phe Pro Ser His Tyr Pro	
1 5	
GAC GAA ACC CTC CGC TCT TTG GCC AGC CCT TCC TCC CTG CAG GGC TCT	758
Asp Glu Thr Leu Arg Ser Leu Ala Ser Pro Ser Ser Leu Gln Gly Ser	
10 15 20 25	
GAG CTC CAC GGC TGG CGC CCC CAA GTG GAC TGT GTC CGG GCC AAT GAG	806
Glu Leu His Gly Trp Arg Pro Gln Val Asp Cys Val Arg Ala Asn Glu	
30 35 40	
CTG TGT GCG GCT GAA TCC AAC TGC AGC TCC AGG TAC CGC ACC CTT CGG	854
Leu Cys Ala Ala Glu Ser Asn Cys Ser Ser Arg Tyr Arg Thr Leu Arg	
45 50 55	
CAG TGC CTG GCA GGC CGG GAT CGC AAT ACC ATG CTG GCC AAT AAG GAG	902
Gln Cys Leu Ala Gly Arg Asp Arg Asn Thr Met Leu Ala Asn Lys Glu	
60 65 70	
TGC CAG GCA GCC CTG GAG GTC TTG CAG GAA AGC CCA CTG TAT GAC TGC	950
Cys Gln Ala Ala Leu Glu Val Leu Gln Glu Ser Pro Leu Tyr Asp Cys	
75 80 85	
CGC TGC AAG CGG GGC ATG AAG AAG GAG CTG CAG TGT CTG CAG ATC TAC	998
Arg Cys Lys Arg Gly Met Lys Lys Glu Leu Gln Cys Leu Gln Ile Tyr	
90 95 100 105	
TGG AGC ATC CAT CTG GGG CTG ACA GAG GGT GAG GAG TTC TAT GAA GCT	1046
Trp Ser Ile His Leu Gly Leu Thr Glu Gly Glu Glu Phe Tyr Glu Ala	
110 115 120	
TCC CCC TAT GAG CCT GTG ACC TCG CGC CTC TCG GAC ATC TTC AGG CTC	1094
Ser Pro Tyr Glu Pro Val Thr Ser Arg Leu Ser Asp Ile Phe Arg Leu	
125 130 135	
GCT TCA ATC TTC TCA GGG ACA GGG ACA GAC CCG GCG GTC AGT ACC AAA	1142
Ala Ser Ile Phe Ser Gly Thr Gly Thr Asp Pro Ala Val Ser Thr Lys	
140 145 150	
AGC AAC CAC TGC CTG GAT GCC GCC AAG GCC TGC AAC CTG AAT GAC AAC	1190
Ser Asn His Cys Leu Asp Ala Ala Lys Ala Cys Asn Leu Asn Asp Asn	
155 160 165	
TGC AAG AAG CTT CGC TCC TCT TAT ATC TCC ATC TGC AAC CGT GAG ATC	1238
Cys Lys Lys Leu Arg Ser Ser Tyr Ile Ser Ile Cys Asn Arg Glu Ile	
170 175 180 185	
TCT CCC ACC GAA CGC TGC AAC CGC CGC AAG TGC CAC AAG GCT CTG CGC	1286
Ser Pro Thr Glu Arg Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg	
190 195 200	
CAG TTC TTT GAC CGT GTG CCC AGC GAG TAT ACC TAC CGC ATG CTC TTC	1334
Gln Phe Phe Asp Arg Val Pro Ser Glu Tyr Thr Tyr Arg Met Leu Phe	
205 210 215	

TGC TCC TGT CAG GAC CAG GCA TGT GCT GAG CGT CGC CGG CAA ACC ATC Cys Ser Cys Gln Asp Gln Ala Cys Ala Glu Arg Arg Arg Gln Thr Ile 220 225 230	1382
CTG CCC AGT TGC TCC TAT GAG GAC AAG GAG AAG CCC AAC TGC CTG GAC Leu Pro Ser Cys Ser Tyr Glu Asp Lys Glu Lys Pro Asn Cys Leu Asp 235 240 245	1430
CTG CGC AGC CTG TGT CGT ACA GAC CAC CTG TGC CGG TCC CGA CTG GCA Leu Arg Ser Leu Cys Arg Thr Asp His Leu Cys Arg Ser Arg Leu Ala 250 255 260 265	1478
GAT TTC CAC GCC AAC TGT CGA GCC TCC TAC CGG ACA ATC ACC AGC TGT Asp Phe His Ala Asn Cys Arg Ala Ser Tyr Arg Thr Ile Thr Ser Cys 270 275 280	1526
CCT GCG GAC AAC TAC CAG GCA TGT CTG GGC TCC TAT GCT GGC ATG ATT Pro Ala Asp Asn Tyr Gln Ala Cys Leu Gly Ser Tyr Ala Gly Met Ile 285 290 295	1574
GGG TTT GAT ATG ACA CCC AAC TAT GTG GAC TCC AAC CCC ACG GGC ATC Gly Phe Asp Met Thr Pro Asn Tyr Val Asp Ser Asn Pro Thr Gly Ile 300 305 310	1622
GTG GTG TCT CCC TGG TGC AAT TGT CGT GGC AGT GGG AAC ATG GAA GAA Val Val Ser Pro Trp Cys Asn Cys Arg Gly Ser Gly Asn Met Glu Glu 315 320 325	1670
GAG TGT GAG AAG TTC CTC AGG GAC TTC ACG GAA AAC CCA TGC CTC CGG Glu Cys Glu Lys Phe Leu Arg Asp Phe Thr Glu Asn Pro Cys Leu Arg 330 335 340 345	1718
AAT GCC ATT CAG GCC TTT GGT AAT GGC ACA GAT GTG AAC ATG TCT CCC Asn Ala Ile Gln Ala Phe Gly Asn Gly Thr Asp Val Asn Met Ser Pro 350 355 360	1766
AAA GGC CCC TCA CTC CCA GCT ACC CAG GCC CCT CGG GTG GAG AAG ACT Lys Gly Pro Ser Leu Pro Ala Thr Gln Ala Pro Arg Val Glu Lys Thr 365 370 375	1814
CCT TCA CTG CCA GAT GAC CTC AGT GAC AGC ACC AGC CTG GGG ACC AGT Pro Ser Leu Pro Asp Asp Leu Ser Asp Ser Thr Ser Leu Gly Thr Ser 380 385 390	1862
GTC ATC ACC ACC TGC ACA TCT ATC CAG GAG CAA GGG CTG AAG GCC AAC Val Ile Thr Thr Cys Thr Ser Ile Gln Glu Gln Gly Leu Lys Ala Asn 395 400 405	1910
AAC TCC AAA GAG TTA AGC ATG TGC TTC ACA GAG CTC ACG ACA AAC ATC Asn Ser Lys Glu Leu Ser Met Cys Phe Thr Glu Leu Thr Thr Asn Ile 410 415 420 425	1958
AGT CCA GGG AGT AAA AAG GTG ATC AAA CTT AAC TCA GGC TCC AGC AGA Ser Pro Gly Ser Lys Lys Val Ile Lys Leu Asn Ser Gly Ser Ser Arg 430 435 440	2006
GCC AGA CTG TCG GCT GCC TTG ACT GCC CTC CCA CTC CTG ATG CTG ACC Ala Arg Leu Ser Ala Ala Leu Thr Ala Leu Pro Leu Leu Met Leu Thr 445 450 455	2054
TTG GCC TTG TAGGCCTTTG GAACCCAGCA CAAAAGTTCT TCAAGCAACC Leu Ala Leu 460	2103

CAGATATGAA CTCCCGCCTG ACAAATGGA AACACACGCA TACACACATG CCACACACAG 2163
 ACACACACAC AGACACACAC ACACACACAC ATACAGACGT CGACGCGGCC GC 2215

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met Leu Val Phe Pro Ser His Tyr Pro Asp Glu Thr Leu Arg Ser Leu
 1 5 10 15
 Ala Ser Pro Ser Ser Leu Gln Gly Ser Glu Leu His Gly Trp Arg Pro
 20 25 30
 Gln Val Asp Cys Val Arg Ala Asn Glu Leu Cys Ala Ala Glu Ser Asn
 35 40 45
 Cys Ser Ser Arg Tyr Arg Thr Leu Arg Gln Cys Leu Ala Gly Arg Asp
 50 55 60
 Arg Asn Thr Met Leu Ala Asn Lys Glu Cys Gln Ala Ala Leu Glu Val
 65 70 75 80
 Leu Gln Glu Ser Pro Leu Tyr Asp Cys Arg Cys Lys Arg Gly Met Lys
 85 90 95
 Lys Glu Leu Gln Cys Leu Gln Ile Tyr Trp Ser Ile His Leu Gly Leu
 100 105 110
 Thr Glu Gly Glu Glu Phe Tyr Glu Ala Ser Pro Tyr Glu Pro Val Thr
 115 120 125
 Ser Arg Leu Ser Asp Ile Phe Arg Leu Ala Ser Ile Phe Ser Gly Thr
 130 135 140
 Gly Thr Asp Pro Ala Val Ser Thr Lys Ser Asn His Cys Leu Asp Ala
 145 150 155 160
 Ala Lys Ala Cys Asn Leu Asn Asp Asn Cys Lys Lys Leu Arg Ser Ser
 165 170 175
 Tyr Ile Ser Ile Cys Asn Arg Glu Ile Ser Pro Thr Glu Arg Cys Asn
 180 185 190
 Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Arg Val Pro
 195 200 205
 Ser Glu Tyr Thr Tyr Arg Met Leu Phe Cys Ser Cys Gln Asp Gln Ala
 210 215 220
 Cys Ala Glu Arg Arg Arg Gln Thr Ile Leu Pro Ser Cys Ser Tyr Glu
 225 230 235 240
 Asp Lys Glu Lys Pro Asn Cys Leu Asp Leu Arg Ser Leu Cys Arg Thr
 245 250 255

Asp His Leu Cys Arg Ser Arg Leu Ala Asp Phe His Ala Asn Cys Arg
 260 265 270
 Ala Ser Tyr Arg Thr Ile Thr Ser Cys Pro Ala Asp Asn Tyr Gln Ala
 275 280 285
 Cys Leu Gly Ser Tyr Ala Gly Met Ile Gly Phe Asp Met Thr Pro Asn
 290 295 300
 Tyr Val Asp Ser Asn Pro Thr Gly Ile Val Val Ser Pro Trp Cys Asn
 305 310 315 320
 Cys Arg Gly Ser Gly Asn Met Glu Glu Glu Cys Glu Lys Phe Leu Arg
 325 330 335
 Asp Phe Thr Glu Asn Pro Cys Leu Arg Asn Ala Ile Gln Ala Phe Gly
 340 345 350
 Asn Gly Thr Asp Val Asn Met Ser Pro Lys Gly Pro Ser Leu Pro Ala
 355 360 365
 Thr Gln Ala Pro Arg Val Glu Lys Thr Pro Ser Leu Pro Asp Asp Leu
 370 375 380
 Ser Asp Ser Thr Ser Leu Gly Thr Ser Val Ile Thr Thr Cys Thr Ser
 385 390 395 400
 Ile Gln Glu Gln Gly Leu Lys Ala Asn Asn Ser Lys Glu Leu Ser Met
 405 410 415
 Cys Phe Thr Glu Leu Thr Thr Asn Ile Ser Pro Gly Ser Lys Lys Val
 420 425 430
 Ile Lys Leu Asn Ser Gly Ser Ser Arg Ala Arg Leu Ser Ala Ala Leu
 435 440 445
 Thr Ala Leu Pro Leu Leu Met Leu Thr Leu Ala Leu
 450 455 460

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1699 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 67..1257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GCGGCCGCGT CGACCGACGC CCAGCACAGG CAGAGCGCTG CCGGGTCCGC GCGTCCAGA	60
CCCGCC ATG GGG CTC TCC CGG AGC CCG CGA CCG CCG CCG CTA GTG ATC	108
Met Gly Leu Ser Arg Ser Pro Arg Pro Pro Pro Leu Val Ile	
1 5 10	
CTG CTA CTG GTG CTG TCG CTG TGG CTA CCC CTT GGA ACA GGA AAC TCC	156

Leu 15	Leu	Leu	Val	Leu	Ser 20	Leu	Trp	Leu	Pro	Leu 25	Gly	Thr	Gly	Asn	Ser 30	
CTT	CCC	ACA	GAG	AAC	AGG	CTT	GTG	AAC	AGC	TGT	ACC	CAG	GCC	AGA	AAA	204
Leu	Pro	Thr	Glu	Asn 35	Arg	Leu	Val	Asn 40	Ser	Cys	Thr	Gln	Ala	Arg 45	Lys	
AAA	TGC	GAG	GCT	AAT	CCC	GCT	TGC	AAG	GCT	GCC	TAC	CAG	CAC	CTG	GAC	252
Lys	Cys	Glu	Ala	Asn 50	Pro	Ala	Cys	Lys 55	Ala	Ala	Tyr	Gln	His 60	Leu	Asp	
TCC	TGC	ACC	CCC	AGT	CTC	AGC	AGT	CCA	CTG	CCC	TCA	GGG	GAG	TCT	GCC	300
Ser	Cys	Thr 65	Pro	Ser	Leu	Ser	Ser 70	Pro	Leu	Pro	Ser	Gly 75	Glu	Ser	Ala	
ACA	TCT	GCA	GCG	TGC	CTT	GAA	GCA	GCA	CAG	CAA	CTC	AGG	AAC	AGC	TCT	348
Thr	Ser	Ala	Ala	Cys	Leu	Glu 85	Ala	Ala	Gln	Gln	Leu	Arg 90	Asn	Ser	Ser	
CTC	ATA	GAC	TGC	AGG	TGC	CAC	CGG	CGC	ATG	AAG	CAC	CAA	GCT	ACC	TGT	396
Leu	Ile	Asp	Cys	Arg	Cys 100	His	Arg	Arg	Met	Lys 105	His	Gln	Ala	Thr 110	Cys	
CTG	GAC	ATT	TAT	TGG	ACC	GTT	CAC	CCT	GTC	CGA	AGC	CTT	GGT	GAC	TAC	444
Leu	Asp	Ile	Tyr	Thr 115	Val	His	Pro	Val 120	Arg	Ser	Leu	Gly 125	Asp	Tyr		
GAG	TTG	GAC	GTC	TCA	CCC	TAT	GAA	GAC	ACA	GTG	ACC	AGC	AAA	CCC	TGG	492
Glu	Leu	Asp	Val	Ser	Pro	Tyr	Glu 135	Asp	Thr	Val	Thr	Ser	Lys 140	Pro	Trp	
AAA	ATG	AAT	CTC	AGC	AAG	CTG	AGC	ATG	CTC	AAA	CCA	GAC	TCC	GAC	CTC	540
Lys	Met	Asn 145	Leu	Ser	Lys	Leu	Ser 150	Met	Leu	Lys	Pro	Asp 155	Ser	Asp	Leu	
TGC	CTC	AAA	TTT	GCT	ATG	CTG	TGT	ACT	CTT	AAC	GAC	AAG	TGC	GAC	CGC	588
Cys	Leu	Lys	Phe	Ala	Met	Leu 165	Cys	Thr	Leu	Asn 170	Asp	Lys	Cys	Asp	Arg	
CTC	CGA	AAG	GCC	TAC	GGG	GAG	GCG	TGC	TCA	GGG	ATC	CGC	TGC	CAG	CGC	636
Leu	Arg	Lys	Ala	Tyr	Gly 180	Glu	Ala	Cys	Ser	Gly 185	Ile	Arg	Cys	Gln 190	Arg	
CAC	CTC	TGC	CTA	GCT	CAG	CTG	GCG	TCC	TTC	TTC	GAG	AAG	GCG	GCA	GAG	684
His	Leu	Cys	Leu	Ala 195	Gln	Leu	Arg	Ser	Phe 200	Phe	Glu	Lys	Ala 205	Ala	Glu	
TCC	CAC	GCT	CAG	GGC	CTG	CTG	CTG	TGT	CCC	TGT	GCA	CCC	GAA	GAT	GCG	732
Ser	His	Ala	Gln 210	Gly	Leu	Leu	Leu 215	Cys	Pro	Cys	Ala	Pro	Glu 220	Asp	Ala	
GGC	TGT	GGG	GAG	CGC	CGG	CGC	AAC	ACC	ATC	GCC	CCC	AGT	TGC	GCC	CTC	780
Gly	Cys	Gly 225	Glu	Arg	Arg	Arg	Asn 230	Thr	Ile	Ala	Pro	Ser 235	Cys	Ala	Leu	
CCG	TCT	GTG	GCC	CCC	AAC	TGC	CTA	GAT	CTT	CGG	AGC	TTC	TGC	CGT	GCG	828
Pro	Ser	Val	Ala	Pro	Asn 245	Cys	Leu	Asp	Leu	Arg	Ser	Phe 250	Cys	Arg	Ala	
GAC	CCT	CTG	TGC	AGA	TCA	CGC	CTG	ATG	GAC	TTC	CAG	ACC	CAC	TGC	CAC	876
Asp	Pro	Leu	Cys	Arg	Ser 260	Arg	Leu	Met	Asp	Phe 265	Gln	Thr	His	Cys 270	His	
CCT	ATG	GAC	ATC	CTC	GGG	ACT	TGT	GCA	ACT	GAG	CAG	TCC	AGA	TGT	CTG	924

Pro Met Asp Ile Leu Gly Thr Cys Ala Thr Glu Gln Ser Arg Cys Leu	
275 280 285	
CGG GCA TAC CTG GGG CTA ATT GGG ACT GCC ATG ACC CCA AAC TTC ATC	972
Arg Ala Tyr Leu Gly Leu Ile Gly Thr Ala Met Thr Pro Asn Phe Ile	
290 295 300	
AGC AAG GTC AAC ACT ACT GTT GCC TTA GGC TGT ACC TGC CGA GGC AGT	1020
Ser Lys Val Asn Thr Thr Val Ala Leu Gly Cys Thr Cys Arg Gly Ser	
305 310 315	
GGC AAC CTG CAG GAC GAG TGT GAA CAG CTG GAA AAG TCC TTC TCC CAG	1068
Gly Asn Leu Gln Asp Glu Cys Glu Gln Leu Glu Lys Ser Phe Ser Gln	
320 325 330	
AAC CCC TGC CTC ATG GAG GCC ATT GCG GCT AAA ATG CGT TTC CAC AGA	1116
Asn Pro Cys Leu Met Glu Ala Ile Ala Ala Lys Met Arg Phe His Arg	
335 340 345 350	
CAA CTC TTC TCC CAG GAC TGG GCG GAC TCT ACT TTT TCT GTG ATG CAG	1164
Gln Leu Phe Ser Gln Asp Trp Ala Asp Ser Thr Phe Ser Val Met Gln	
355 360 365	
CAG CAG AAC AGC AGC CCT GCT CTG AGG CCC CAG CTC AGG CTA CCC GTT	1212
Gln Gln Asn Ser Ser Pro Ala Leu Arg Pro Gln Leu Arg Leu Pro Val	
370 375 380	
CTG TCT TTC TTC ATC CTT ACC TTG ATT CTG CTG CAG ACC CTC TGG	1257
Leu Ser Phe Ile Leu Thr Leu Ile Leu Leu Gln Thr Leu Trp	
385 390 395	
TAAC TGGGCT CCCTCAGGGT CCTTTGTCCT CTCCACCACA CCCAGACCGA CTTGCAGCCT	1317
GTGATGGGAG AGAAAATGCT GGCCTCTGGA AGAAGATGCA ACCAGGCTCA CTGCACATCC	1377
TGTCTGCTCC AGATGAGGTC TTGGAAGAAG CGAGGGCTGT GACCGTTCAG AATCCTGAGC	1437
GGCCAGCTTT CAAACCTCTC CTACTTACTC CTGCTTGGGC TGCTCCTCCC TAGGACCTTG	1497
TACTCCAGTT TGCGTGATA TTGTGGTGGT GATTAGCTTC CCACCTCCAG CCCTTCTTCC	1557
TGTTTCCCAG GACCACCCAG GGCTAATGAC TCACTCATTC CTGGTTGCCT TCTCCAGGAA	1617
GGCAGGCTGA GGTTCTGAG GCAGCTGAGA AAGATGGTCC CTTTGTGAGG AAGGCTGGTG	1677
GTCCAACCGT CGACGCGGCC GC	1699

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 397 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met Gly Leu Ser Arg Ser Pro Arg Pro Pro Pro Leu Val Ile Leu Leu	
1 5 10 15	
Leu Val Leu Ser Leu Trp Leu Pro Leu Gly Thr Gly Asn Ser Leu Pro	
20 25 30	

Thr Glu Asn Arg Leu Val Asn Ser Cys Thr Gln Ala Arg Lys Lys Cys
 35 40 45
 Glu Ala Asn Pro Ala Cys Lys Ala Ala Tyr Gln His Leu Asp Ser Cys
 50 55 60
 Thr Pro Ser Leu Ser Ser Pro Leu Pro Ser Gly Glu Ser Ala Thr Ser
 65 70 75 80
 Ala Ala Cys Leu Glu Ala Ala Gln Gln Leu Arg Asn Ser Ser Leu Ile
 85 90 95
 Asp Cys Arg Cys His Arg Arg Met Lys His Gln Ala Thr Cys Leu Asp
 100 105 110
 Ile Tyr Trp Thr Val His Pro Val Arg Ser Leu Gly Asp Tyr Glu Leu
 115 120 125
 Asp Val Ser Pro Tyr Glu Asp Thr Val Thr Ser Lys Pro Trp Lys Met
 130 135 140
 Asn Leu Ser Lys Leu Ser Met Leu Lys Pro Asp Ser Asp Leu Cys Leu
 145 150 155 160
 Lys Phe Ala Met Leu Cys Thr Leu Asn Asp Lys Cys Asp Arg Leu Arg
 165 170 175
 Lys Ala Tyr Gly Glu Ala Cys Ser Gly Ile Arg Cys Gln Arg His Leu
 180 185 190
 Cys Leu Ala Gln Leu Arg Ser Phe Phe Glu Lys Ala Ala Glu Ser His
 195 200 205
 Ala Gln Gly Leu Leu Leu Cys Pro Cys Ala Pro Glu Asp Ala Gly Cys
 210 215 220
 Gly Glu Arg Arg Arg Asn Thr Ile Ala Pro Ser Cys Ala Leu Pro Ser
 225 230 235 240
 Val Ala Pro Asn Cys Leu Asp Leu Arg Ser Phe Cys Arg Ala Asp Pro
 245 250 255
 Leu Cys Arg Ser Arg Leu Met Asp Phe Gln Thr His Cys His Pro Met
 260 265 270
 Asp Ile Leu Gly Thr Cys Ala Thr Glu Gln Ser Arg Cys Leu Arg Ala
 275 280 285
 Tyr Leu Gly Leu Ile Gly Thr Ala Met Thr Pro Asn Phe Ile Ser Lys
 290 295 300
 Val Asn Thr Thr Val Ala Leu Gly Cys Thr Cys Arg Gly Ser Gly Asn
 305 310 315 320
 Leu Gln Asp Glu Cys Glu Gln Leu Glu Lys Ser Phe Ser Gln Asn Pro
 325 330 335
 Cys Leu Met Glu Ala Ile Ala Ala Lys Met Arg Phe His Arg Gln Leu
 340 345 350
 Phe Ser Gln Asp Trp Ala Asp Ser Thr Phe Ser Val Met Gln Gln Gln
 355 360 365

Asn Ser Ser Pro Ala Leu Arg Pro Gln Leu Arg Leu Pro Val Leu Ser
 370 375 380

Phe Phe Ile Leu Thr Leu Ile Leu Leu Gln Thr Leu Trp
 385 390 395

(2) INFORMATION FOR SEQ ID NO:43:..

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 498 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Met	Val	Xaa	Xaa	Leu	Xaa	Xaa	Xaa	Pro	Xaa	Pro	Pro	Xaa	Xaa	Xaa	Met
1				5				10						15	
Xaa	Leu	Xaa	Leu	Leu	Ser	Leu	Ala	Leu	Pro	Leu	Xaa	Xaa	Xaa	Leu	Gln
			20					25						30	
Gly	Ala	Glu	Leu	Xaa	Gly	Xaa	Xaa	Arg	Leu	Xaa	Xaa	Asp	Cys	Val	Xaa
		35					40					45			
Ala	Xaa	Xaa	Xaa	Cys	Xaa	Ala	Glu	Xaa	Xaa	Cys	Ser	Xaa	Xaa	Tyr	Arg
	50					55					60				
Thr	Leu	Arg	Gln	Cys	Xaa	Ala	Gly	Xaa	Xaa	Xaa	Asn	Thr	Xaa	Leu	Ala
65				70						75				80	
Ser	Gly	Xaa	Glu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Ala	Xaa	Glu
			85					90						95	
Xaa	Leu	Xaa	Xaa	Ser	Ser	Leu	Tyr	Asp	Cys	Arg	Cys	Lys	Arg	Gly	Met
			100					105					110		
Lys	Lys	Glu	Xaa	Xaa	Cys	Leu	Xaa	Ile	Tyr	Trp	Ser	Xaa	His	Xaa	Xaa
		115				120						125			
Leu	Xaa	Xaa	Gly	Asn	Xaa	Xaa	Leu	Glu	Xaa	Ser	Pro	Tyr	Glu	Pro	Xaa
	130				135						140				
Val	Thr	Ser	Arg	Leu	Ser	Asp	Ile	Phe	Arg	Xaa	Xaa	Ser	Xaa	Xaa	Ser
145				150					155						160
Xaa	Xaa	Xaa	Xaa	Asp	Xaa	Xaa	Xaa	Xaa	Xaa	Lys	Ser	Asn	Xaa	Cys	Leu
				165				170						175	
Asp	Ala	Ala	Lys	Ala	Cys	Asn	Leu	Asn	Asp	Xaa	Cys	Lys	Lys	Leu	Arg
			180					185					190		
Ser	Ala	Tyr	Ile	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Ser	Xaa	Xaa	Glu	Arg
		195				200						205			
Cys	Asn	Arg	Arg	Lys	Cys	His	Lys	Ala	Leu	Arg	Gln	Phe	Phe	Asp	Lys
	210					215					220				
Val	Pro	Xaa	Xaa	His	Xaa	Tyr	Gly	Met	Leu	Phe	Cys	Ser	Cys	Xaa	Xaa

225		230		235		240
Xaa Asp Xaa Ala Cys	Xaa Glu Arg Arg Arg Gln Thr Ile Xaa Pro Ser					
	245		250		255	
Cys Ser Tyr Glu Xaa Xaa Glu Lys Pro Asn Cys Leu Asp Leu Arg Xaa						
	260		265		270	
Xaa Cys Arg Thr Asp Xaa Leu Cys Arg Ser Arg Leu Ala Asp Phe Xaa						
	275		280		285	
Thr Asn Cys Xaa Xaa Xaa Xaa Arg Xaa Val Xaa Ser Cys Xaa Ala Xaa						
	290		295		300	
Asn Tyr Xaa Xaa Cys Leu Xaa Ala Tyr Xaa Gly Leu Ile Gly Thr Xaa						
	305		310		315	
Met Thr Pro Asn Tyr Val Asp Ser Ser Xaa Thr Xaa Xaa Xaa Val Ala						
	325		330		335	
Pro Trp Cys Xaa Cys Arg Gly Ser Gly Asn Xaa Xaa Glu Glu Cys Glu						
	340		345		350	
Lys Phe Leu Xaa Phe Phe Xaa Xaa Asn Pro Cys Leu Xaa Asn Ala Ile						
	355		360		365	
Gln Ala Phe Gly Asn Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa						
	370		375		380	
Xaa Pro Xaa Phe Ser Val Xaa Xaa Xaa Xaa Xaa Thr Xaa Thr Xaa Ala						
	385		390		395	
Xaa Arg Val Xaa Xaa Xaa Pro Ser Leu Xaa Xaa Xaa Xaa Ser Xaa Xaa						
	405		410		415	
Xaa Xaa Leu Xaa Thr Xaa Val Xaa Xaa Xaa Cys Xaa Xaa Leu Gln Xaa						
	420		425		430	
Gln Xaa Leu Lys Xaa Asn Xaa Ser Xaa Glu Xaa Xaa Xaa Cys Phe Xaa						
	435		440		445	
Glu Leu Thr Thr Asn Xaa Xaa Xaa Xaa Ser Gly Xaa Xaa Xaa Xaa Ile						
	450		455		460	
Xaa Xaa Xaa Ser Xaa Xaa Ala Xaa Pro Ser Xaa Ala Leu Xaa Xaa Leu						
	465		470		475	
Pro Val Leu Met Leu Thr Ala Leu Ala Xaa Leu Leu Ser Xaa Xaa Xaa						
	485		490		495	
Xaa Ser						

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 489 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa Leu Xaa
 1 5 10 15
 Thr Leu Xaa Ser Leu Xaa Xaa Pro Leu Xaa Leu Xaa Xaa Ser Xaa Xaa
 20 25 30
 Xaa Xaa Xaa Arg Xaa Xaa Xaa Asp Cys Val Xaa Ala Xaa Xaa Xaa Cys
 35 40 45
 Xaa Ala Glu Xaa Xaa Cys Ser Xaa Xaa Tyr Arg Thr Leu Arg Gln Cys
 50 55 60
 Xaa Ala Gly Xaa Xaa Xaa Asn Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ala
 65 70 75 80
 Xaa Xaa Glu Cys Xaa Xaa Ala Xaa Glu Xaa Leu Xaa Xaa Ser Ser Leu
 85 90 95
 Tyr Asp Cys Arg Cys Lys Arg Gly Met Lys Lys Glu Xaa Xaa Cys Leu
 100 105 110
 Xaa Ile Tyr Trp Ser Xaa His Xaa Xaa Leu Xaa Xaa Gly Xaa Xaa Xaa
 115 120 125
 Leu Glu Xaa Ser Pro Tyr Glu Xaa Pro Val Thr Ser Arg Leu Ser Asp
 130 135 140
 Ile Phe Arg Xaa Xaa Ser Xaa Xaa Ser Xaa Xaa Xaa Xaa Asp Xaa Xaa
 145 150 155 160
 Xaa Xaa Xaa Lys Ser Asn Xaa Cys Leu Asp Ala Ala Lys Ala Cys Asn
 165 170 175
 Leu Asn Asp Xaa Cys Lys Lys Leu Arg Ser Ala Tyr Ile Xaa Xaa Cys
 180 185 190
 Xaa Xaa Xaa Xaa Ser Xaa Xaa Glu Arg Cys Asn Arg Arg Lys Cys His
 195 200 205
 Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Xaa Xaa His Xaa Tyr
 210 215 220
 Gly Met Leu Phe Cys Ser Cys Xaa Xaa Xaa Asp Xaa Ala Cys Xaa Glu
 225 230 235 240
 Arg Arg Arg Gln Thr Ile Xaa Pro Ser Cys Ser Tyr Glu Xaa Xaa Glu
 245 250 255
 Xaa Pro Asn Cys Leu Asp Leu Arg Ser Xaa Cys Arg Thr Asp Xaa Leu
 260 265 270
 Cys Arg Ser Arg Leu Ala Asp Phe Xaa Thr Asn Cys Xaa Pro Xaa Xaa
 275 280 285
 Arg Xaa Xaa Thr Xaa Cys Xaa Ala Xaa Asn Tyr Xaa Xaa Cys Leu Xaa
 290 295 300
 Ala Tyr Xaa Gly Leu Ile Gly Thr Xaa Met Thr Pro Asn Tyr Val Asp
 305 310 315 320

Ser Xaa Xaa Thr Xaa Xaa Xaa Val Ala Pro Trp Cys Xaa Cys Arg Gly
 325 330 335
 Ser Gly Asn Xaa Xaa Glu Glu Cys Glu Lys Phe Leu Xaa Xaa Phe Xaa
 340 345 350
 Xaa Asn Pro Cys Leu Xaa Asn Ala Ile Gln Ala Phe Gly Asn Gly Xaa
 355 360 365
 Asp Val Xaa Met Ser Gln Xaa Xaa Pro Xaa Xaa Xaa Xaa Thr Xaa Ala
 370 375 380
 Xaa Xaa Xaa Xaa Xaa Xaa Arg Val Xaa Xaa Xaa Pro Xaa Leu Xaa Xaa
 385 390 395 400
 Xaa Xaa Ser Xaa Xaa Xaa Xaa Xaa Xaa Thr Xaa Val Xaa Xaa Xaa Cys
 405 410 415
 Xaa Xaa Xaa Gln Xaa Gln Xaa Leu Lys Xaa Asn Xaa Ser Xaa Xaa Xaa
 420 425 430
 Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 435 440 445
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Xaa Xaa Ala Xaa Xaa Ser Xaa
 450 455 460
 Xaa Leu Xaa Xaa Leu Pro Val Leu Met Leu Thr Xaa Leu Xaa Xaa Xaa
 465 470 475 480
 Leu Xaa Xaa Xaa Leu Xaa Glu Thr Ser
 485

CLAIMS

What is claimed is:

- 5 1. An isolated and purified protein comprising an amino acid sequence as depicted in Figure 2 or 4 (SEQ ID NO: 2 or 4) and analogs thereof wherein the protein is capable of complexing with glial cell line-derived neurotrophic factor (GDNF) and thereby mediating cell response to GDNF.
- 10 2. A protein of Claim 1 comprising the amino acid sequence as depicted in Figure 2 (SEQ ID NO: 2).
3. A protein of Claim 1 comprising the amino acid sequence as depicted in Figure 4 (SEQ ID NO:4).
- 15 4. A protein of Claim 1 comprising the amino acid sequence Ser¹⁸ through Pro⁴⁴⁶ as depicted in Figure 2 (SEQ ID NO:2).
5. A protein of Claim 1 comprising the amino acid sequence Asp²⁵ through
20 Leu⁴⁴⁷ as depicted in Figure 2 (SEQ ID NO:2).
6. A protein of Claim 1 comprising the amino acid sequence Cys²⁹ through Cys⁴⁴² as depicted in Figure 2 (SEQ ID NO:2).
- 25 7. A protein of Claim 1 comprising the amino acid sequence Ala¹⁹ through Val⁴⁵⁰ as depicted in Figure 4 (SEQ ID NO:4).
8. A protein of Claim 1 comprising the amino acid sequence Cys²⁹ through Cys⁴⁴³ as depicted in Figure 4 (SEQ ID NO:4).
- 30 9. A protein of Claim 1 which is glycosylated.
10. A protein of Claim 1 which is non-glycosylated.
- 35 11. A protein of Claims 1 to 10 which is produced by recombinant technology or chemical synthesis.

12. A pharmaceutical composition comprising a protein as claimed in any one of claims 1 to 10 in combination with a pharmaceutically acceptable carrier.
13. An isolated nucleic acid sequence encoding a neurotrophic factor receptor protein comprising an amino acid sequence as claimed in any one of claims 1 to 8.
14. An isolated nucleic acid sequence encoding a neurotrophic factor receptor protein comprising an amino acid sequence as depicted in Figure 2 or 4 (SEQ ID NO: 2 or 4) and analogs thereof wherein the protein is capable of complexing with glial cell line-derived neurotrophic factor (GDNF) and thereby mediating cell response to GDNF.
15. A nucleic acid sequence of Claim 14 encoding a neurotrophic factor receptor protein comprising the amino acid sequence as depicted in Figure 2 (SEQ ID NO: 2).
16. A nucleic acid sequence of Claim 14 encoding a neurotrophic factor receptor protein comprising the amino acid sequence as depicted in Figure 4 (SEQ ID NO: 4).
17. An isolated nucleic acid sequence comprising:
- a sequence set forth in Figure 1 (SEQ ID NO: 1) comprising nucleotides encoding Met¹ through Ser⁴⁶⁵ or Figure 3 (SEQ ID NO: 3) comprising nucleotides encoding Met¹ through Ser⁴⁶⁸, wherein said sequence encodes a neurotrophic factor receptor protein (GDNFR) capable of complexing with glial cell line-derived neurotrophic factor (GDNF) and thereby mediating cell response to GDNF;
 - a nucleic acid sequence which (1) hybridizes to a complementary sequence of (a) and (2) encodes an amino acid sequence with GDNFR activity; and
 - a nucleic acid sequence which but for the degeneracy of the genetic code would hybridize to a complementary sequence of (a) and (2) encodes an amino acid sequence with GDNFR activity.
18. A vector comprising a nucleic acid sequence according to any of claims 14 to 17 operatively linked to one or more operational elements capable of effecting the amplification or expression of said nucleic acid sequence.
19. A vector comprising a nucleic acid sequence encoding a neurotrophic factor receptor protein comprising the amino acid sequence as depicted in Figure 2 or 4

(SEQ ID NO: 2 or 4) operatively linked to one or more operational elements capable of effecting the amplification or expression of said nucleic acid sequence.

20. A host cell transformed or transfected with the vector of claim 18.
- 5 21. A host cell transformed or transfected with the vector of claim 19.
22. A host cell of claim 20 selected from the group consisting of mammalian cells and bacterial cells.
- 10 23. A host cell of claim 22 which is a COS-7 cell or E. coli.
24. A host cell of Claim 20 wherein said cell is suitable for human implantation and wherein said cell expresses and secretes said neurotrophic factor receptor.
- 15 25. A host cell of Claim 21 wherein said cell is suitable for human implantation and wherein said cell expresses and secretes said neurotrophic factor receptor.
26. A host cell of Claim 20 wherein said cell is transformed or transfected ex vivo.
- 20 27. A host cell of Claim 20 wherein said cell is enclosed in a semipermeable membrane suitable for human implantation.
- 25 28. A method for the production of a neurotrophic factor receptor protein comprising the steps of:
- (a) culturing a host cell, containing a nucleic acid sequence encoding a neurotrophic factor receptor protein comprising an amino acid sequence as depicted in Figure 2 or 4 (SEQ ID NO: 2 or 4) and analogs thereof wherein the protein is capable of complexing with glial cell line-derived neurotrophic factor (GDNF) and thereby mediating cell response to GDNF, under conditions suitable for the expression of said neurotrophic factor receptor protein by said host cell; and
- 30 (b) optionally, isolating said neurotrophic factor receptor protein expressed by said host cell.
- 35 29. A method of claim 28, wherein said nucleic acid sequence encodes a

neurotrophic factor receptor protein comprising the amino acid sequence as depicted in Figure 2 (SEQ ID NO:2).

30. A method of claim 28, wherein said nucleic acid sequence encodes a
5 neurotrophic factor receptor protein comprising the amino acid sequence as depicted in Figure 4 (SEQ ID NO:4).

31. A method for the production of a neurotrophic factor receptor protein comprising the steps of:

- 10 (a) culturing a host cell transformed or transfected with a nucleic acid sequence according to claim 17 under conditions suitable for the expression of said neurotrophic factor receptor protein by said host cell; and
(b) optionally, isolating said neurotrophic factor receptor protein expressed by said host cell.

15

32. A method of claim 28 or 31, further comprising the step of refolding the isolated neurotrophic factor receptor.

33. A method of claim 28 or 31, wherein said host cell is a prokaryotic cell.

20

34. A method of claim 28 or 31, wherein said host cell is a eukaryotic cell.

35. A substantially purified neurotrophic factor receptor protein prepared according to the method of any of claims 28 to 31.

25

36. The use of the neurotrophic factor receptor protein of claim 1 for the manufacture of a pharmaceutical composition.

37. A method of treating improperly functioning dopaminergic nerve cells by
30 administering a neurotrophic factor receptor protein of claim 1.

38. A method of treating Parkinson's disease by administering a neurotrophic factor receptor protein of claim 1.

35 39. A method of treating Alzheimer's disease by administering a neurotrophic factor receptor protein of claim 1.

40. A method of treating amyotrophic lateral sclerosis by administering a neurotrophic protein of claim 1.
41. An antibody that binds to a neurotrophic factor receptor protein comprising
5 an amino acid sequence of SEQ ID NO:2 or SEQ ID NO:4.
42. The antibody of claim 41 wherein said antibody is a monoclonal antibody.
43. The antibody of claim 41 wherein said antibody is a polyclonal antibody.
- 10 44. An antibody produced by immunizing an animal with a neurotrophic factor receptor protein comprising an amino acid sequence of SEQ ID NO:2 or SEQ ID NO:4.
- 15 45. A hybridoma that produces a monoclonal antibody that binds to a neurotrophic factor receptor protein comprising an amino acid sequence of SEQ ID NO:2 or SEQ ID NO:4.
46. A device for treating nerve damage, comprising:
20 (a) a semipermeable membrane suitable for implantation; and
(b) cells encapsulated within said membrane, wherein said cells secrete a neurotrophic factor receptor protein according to claim 1;
said membrane being permeable to the neurotrophic factor receptor protein and impermeable to materials detrimental to said cells.
- 25 47. The device of claim 46, wherein said cells are naturally occurring cells that secrete said neurotrophic factor receptor protein.
48. The device of claim 46, wherein said cells have been modified to secrete said
30 neurotrophic factor receptor protein by means of a nucleic acid sequence comprising:
(a) a sequence set forth in Figure 1 (SEQ ID NO.: 1) comprising nucleotides encoding Met¹ through Ser⁴⁶⁵ or Figure 3 (SEQ ID NO: 3) comprising nucleotides encoding Met¹ through Ser⁴⁶⁸ encoding a neurotrophic factor receptor protein (GDNFR) capable of complexing with glial cell line-derived
35 neurotrophic factor (GDNF) and mediating cell response to GDNF;
(b) a nucleic acid sequence which (1) hybridizes to a complementary sequence of

- (a) and (2) encodes an amino acid sequence with GDNFR activity; and
(c) a nucleic acid sequence which but for the degeneracy of the genetic code would hybridize to a complementary sequence of (a) and (2) encodes an amino acid sequence with GDNFR activity.

5

49. An assay device for analyzing a test sample for the presence of glial cell line-derived neurotrophic factor, comprising: a solid phase containing or coated with a GDNFR protein, wherein said GDNFR protein reacts with GDNF present in the test sample and produces a detectable reaction product indicative of the presence of GDNF.

10

50. A method for analyzing a test sample for the presence of glial cell line-derived neurotrophic factor, comprising: contacting the sample to an assay reagent comprising GDNFR protein, wherein said GDNFR protein reacts with GDNF present in the test sample and produces a detectable reaction product indicative of the presence of GDNF.

15

51. An isolated and purified protein comprising an amino acid sequence of GDNFR- α , GRR2, GRR3 or GDNFR consensus protein as depicted in Figure 14, 15, 16, 17, 18, 19 or 26 wherein the protein is capable of complexing with glial cell line-derived neurotrophic factor (GDNF) or neurturin neurotrophic factor thereby mediating cell response to said neurotrophic factor.

20

52. A pharmaceutical composition comprising a protein as claimed in claim 51 in combination with a pharmaceutically acceptable carrier.

25

53. An isolated nucleic acid sequence encoding a neurotrophic factor receptor protein comprising an amino acid sequence claim 51.

30 54. An isolated nucleic acid sequence comprising:

- (a) a sequence set forth in Figure 19 or 26 wherein said sequence encodes a neurotrophic factor receptor protein (GDNFR) capable of complexing with glial cell line-derived neurotrophic factor (GDNF) or neurturin neurotrophic factor thereby mediating cell response to said neurotrophic factor;
- (b) a nucleic acid sequence which (1) hybridizes to a complementary sequence of (a) and (2) encodes an amino acid sequence with GDNFR activity; and

35

- (c) a nucleic acid sequence which but for the degeneracy of the genetic code would hybridize to a complementary sequence of (a) and (2) encodes an amino acid sequence with GDNFR activity.

- 5 55. A vector comprising a nucleic acid sequence according claims 53 or 54 operatively linked to one or more operational elements capable of effecting the amplification or expression of said nucleic acid sequence.
56. A host cell transformed or transfected with the vector of claim 55.
- 10 57. A host cell of Claim 56 wherein said cell is suitable for human implantation and wherein said cell expresses and secretes said neurotrophic factor receptor.
58. A host cell of Claim 56 wherein said cell is transformed or transfected ex vivo.
- 15 59. A host cell of Claim 56 wherein said cell is enclosed in a semipermeable membrane suitable for human implantation.
- 20 60. A method for the production of a neurotrophic factor receptor protein comprising the steps of:
- (a) culturing a host cell, containing a nucleic acid sequence encoding a neurotrophic factor receptor protein comprising an amino acid sequence of claim 51 wherein the protein is capable of complexing with glial cell line-
- 25 derived neurotrophic factor (GDNF) or neurturin neurotrophic factor thereby mediating cell response to said neurotrophic factor, under conditions suitable for the expression of said neurotrophic factor receptor protein by said host cell; and
- (b) optionally, isolating said neurotrophic factor receptor protein expressed by
- 30 said host cell.
61. A method of treating improperly functioning dopaminergic nerve cells by administering a neurotrophic factor receptor protein of claim 51.
- 35 62. An antibody that binds to a neurotrophic factor receptor protein comprising an amino acid sequence of claim 51.

63. A hybridoma that produces a monoclonal antibody that binds to a neurotrophic factor receptor protein comprising an amino acid sequence of claim 51.

64. A device for treating nerve damage, comprising:

- 5 (a) a semipermeable membrane suitable for implantation; and
(b) cells encapsulated within said membrane, wherein said cells secrete a neurotrophic factor receptor protein according to claim 51;
said membrane being permeable to the neurotrophic factor receptor protein and impermeable to materials detrimental to said cells.

10

65. An assay device for analyzing a test sample for the presence of a neurotrophic factor, comprising: a solid phase containing or coated with a GDNFR protein, wherein said GDNFR protein reacts with said neurotrophic factor present in the test sample and produces a detectable reaction product indicative of the presence
15 of neurotrophic factor.

15

66. A method for analyzing a test sample for the presence of a neurotrophic factor, comprising: contacting the sample to an assay reagent comprising GDNFR protein, wherein said GDNFR protein reacts with said neurotrophic factor present in
20 the test sample and produces a detectable reaction product indicative of the presence of neurotrophic factor.

20

67. A method of determining whether a ligand activates a receptor tyrosine kinase, comprising: contacting the sample to an assay reagent comprising GDNFR
25 protein, wherein said GDNFR protein reacts with said ligand to form a GDNFR protein/ligand complex and wherein said complex binds to an extracellular ligand-binding domain of said receptor tyrosine kinase, and detecting the activation of the kinase domain and phosphorylation of specific substrates that mediate intracellular signaling.

30

68. A method of claim 67, wherein said receptor tyrosine kinase is a c-ret proto-oncogene.

69. A method of claim 67, wherein a cell has been modified to include the
35 extracellular ligand-binding domain, a transmembrane domain and a cytoplasmic segment containing the catalytic protein-tyrosine kinase domain for the detection of intracellular signaling.

35

Human Glial Cell Line-Derived Neurotrophic Factor Receptor Protein

1 / 1 3 5

10	30	50
AATCTGGCCTCGGAACACGCCATTCTCCGCGCCGCTTCCAATAACCACTAACATCCCCTA		
70	90	110
ACGAGCATCCGAGCCGAGGGCTCTGCTCGGAAATCGTCTGGCCCAACTCGGCCCTTCGA		
130	150	170
GCTCTCGAAGATTACCGCATCTATTTTTTTTCTTTTCTTTTCTTTTCTTTCTAGCGCAGATA		

FIG. 1B

190 210 230
AAGTGAGCCCCGGAAGGAGGGGGGACACCATGCCCCTGAAAGAAATAATAA

250 270 290
GTAAATAACAACCTGGCTCCTCGCCGACGCTGGACGCGGTGAGTCCAGGTTGGG

310 330 350
TCGGACCTGAACCCCTAAAGCGGAACCGCCTCCCGCCCTCGCCATCCCGGAGCTGAGTC

370 390 410
GCCGGCGCGGTGGCTGCTGCCAGACCCGGAGTTTCCTCTTCACTGGATGGAGCTGAAC

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FIG.1C

430	450	470
TTTGGGCGCCAGAGCAGCACAGCTGTCCGGGGATCGCTGCACGCTGAGCTCCCTCGGCA		
490	510	530
AGACCCAGCGCGGCTCGGGATTTTTGGGGGGCGGGACCCAGCCCCGCGCGGCACC		
550	570	590
ATGTTCCCTGGCGACCCCTGTACTTCGCGGCTGCCGCTCTTGGA		
CTCCTGTCGGCCGAA		
M	F	L
A	T	L
A	Y	F
T	A	L
L	P	L
L	L	D
L	L	L
L	L	L
S	A	A
E		

FIG.1D

610 630 650
GTGAGCGCGGAGACCGCCTGGATTGCCGTGAAAGCCAGTGATCAGTGCCCTGAAGGAGCAG
V S G G D R L D C V K A S D Q C L K E Q

670 690 710
AGCTGCAGCACCAAGTACCGCACGCTAAGGCAGTGCGTGGCGGGCAAGGAGACCACTTC
S C S T K Y R T L R Q C V A G K E T N F

730 750 770
AGCCTGGCATCCGGCCTGGAGGCCAAGGATGAGTGCCGCAGCGCCCATGGAGGCCCTGAAG
S L A S G L E A K D E C R S A M E A L K

FIG. 1E

790 810 830
CAGAAGTCGCTCTAACAAGTCCCGCTGCAAGCGGGGTATGAAGAAGGAGAACTGCCTG
Q K S L Y N C R C K R G M K K E K N C L

850 870 890
CGCATTTACTGGAGCATGTACCAGAGCCCTGCAGGGAAATGATCTGCTGGAGGATTCCCCA
R I Y W S M Y Q S L Q G N D L L E D S P

910 930 950
TATGAACCAGTTAACAGCAGATGTCAGATATATTCGGGGTGGTCCCATTCATATCAGAT
Y E P V N S R L S D I F R V V P F I S D

FIG.1F

970 990 1010
GTTTTTCAGCAAGTGGAGCACATTCCCAAGGGAACAACCTGCCTGGATGCAGCGAAGGCC
V F Q Q V E H I P K G N N C L D A A K A

1030 1050 1070
TGCAACCTCGACGACATTTGCAAGAAGTACAGGTCGGCGGTACATCACCCCGTGCACCCACC
C N L D D I C K K Y R S A Y I T P C T T

1090 1110 1130
AGCGTGTCCAACGATGTCTGCAACCGCCGCAAGTGCCACAAGGCCCTCCGGCAGTTCITT
S V S N D V C N R R K C H K A L R Q F F

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FIG.1G

1150	1170	1190
GACAAGGTCCTCCGGCCAAAGCACAGCTACGGAATGCTCTTCTGTCTCCTGCCGGGACATCGCC		
D K V P A K H S Y G M L F C S C R D I A		
1210	1230	1250
TGCACAGAGCGGAGCGCACAGACCATCGTGCCGTGTGTCTCCTATGAAGAGAGGAGAAG		
C T E R R R Q T I V P V C S Y E E R E K		
1270	1290	1310
CCCAACTGTTTGAATTTCAGGACTCCTGCAAGACGGAATTACATCTGCAGATCTCGCCTT		
P N C L N L Q D S C K T N Y I C R S R L		

FIG.1H

1330 1350 1370
GCGGATTTTACCAACTGCCAGCCAGAGTCAAGGCTCTGTCAGCAGCTGTCTAAAGGAA
A D F F T N C Q P E S R S V S S C L K E

1390 1410 1430
AACTACGCTGACTGCCCTCCTCGCCCTACTCGGGGCTTATTGGCACAGTCATGACCCCAAC
N Y A D C L L A Y S G L I G T V M T P N

1450 1470 1490
TACATAGACTCCAGTAGCCTCAGTGTGGCCCCCATGGTGTGACTGCAGCAACAGTGGGAAC
Y I D S S S L S V A P W C D C S N S G N

FIG. 11

1510	1530	1550
GACCTAGAAGAGTGCTTGAAATTTTGAATTTCTTCAAGGACAATACATGCTCTTAAAAAT		
D L E E C L K F L N F F K D N T C L K N		
1570	1590	1610
GCAATTCAAGCCTTTGGCAATGGCTCCGATGTGACCGTGTGGCAGCCAGCCTTCCCAGTA		
A I Q A F G N G S D V T V W Q P A F P V		
1630	1650	1670
CAGACCACCACTGCCACTACCACCACCTGCCCTCCGGTTAAGAACAAGCCCCCTGGGGCCA		
Q T T A T T T A L R V K N K P L G P		

FIG. 1J

1690 1710 1730
GCAGGGTCTGAGAAATGAAATTCCTCACTCATGTTTGGCCACCGTGTGCAAAATTACAGGCA
A G S E N E I P T H V L P P C A N L Q A

1750 1770 1790
CAGAAGCTGAAATCCAATGTGTCGGGCAATACACACCTCTGTATTTCCAATGGTAATTAT
Q K L K S N V S G N T H L C I S N G N Y

1810 1830 1850
GAAAAAGAGGTCTCGGTGCTTCCAGCCACATAACCAAAATCAATGGCTGCTCCTCCA
E K E G L G A S S H I T T K S M A A P P

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FIG. 1K

1870 1890 1910
AGCTGTGGTCTGAGCCCACTGCTGGTCCTGGTGGTAACCGCTCTGTCCACCCCTATTATCT
S C G L S P L L V L V V T A L S T L L S
1930 1950 1970
TTAACAGAAACATCATAGCTGCATTAAAAAATACAATATGGACATGTAAAAAGACAAA
L T E T S *
1990 2010 2030
ACCAAGTTATCTGTTTCCTGTTCTCTTGTATAGCTGAAATTCCAGTTTAGGAGCTCAGTT
2050 2070 2090
GAGAAACAGTTCATTCAACTGGAACATTTTTTTTTTTT.CCTTTTAAGAAAGCTTCTTGT

1 2 / 1 3 5

FIG. 1L

2110 2130 2150
GATCCCTT.GGGGCTTCTGTGAAAAACCTGATGCAGTGCTCCATCCAAACTCAGAAGGCTT

2170 2190 2210
TGGGATATGCTGTATTTTAAAGGGACAGTTTGTAACTTGGGCTGTAAAGCAAACCTGGGCGC

2230 2250 2270
TGTGTTTTCGATGATGATGAT.ATCATGAT.ATGAT.....

2290 2310 2330
.....GATTTAACAGTTTACTTCTGGCCTTTCCTAGCTAGAGAGGAG

FIG. 1M

2350 2370 2390
TTAATATTCTAAGGTAACCTCCCATATCTCCTTTTAATGACATTGATTTCTAATGATATAA

2410 2430 2450
ATTTCAGCCTACATTGATGCCAAGCTTTTGTGCCACAAGAAGATTCTTACCAAGAGTGG

2470 2490 2510
GCTTTGTGGAACAGCTGGTACTGATGTTTACCTTTTATATATGTACTAGCATTTTCCACG

2530 2550
CTGATGTTTATGTACTGTAAACAGTTCTGCACTCTTGTACAAAAGAAA

FIG.2A

Human Glial Cell Line-Derived
Neurotrophic Factor Receptor Protein

M	F	L	A	T	L	Y	F	A	L	P	L	L	D	L	L	L	S	A	E	20
V	S	G	G	D	R	L	D	C	V	K	A	S	D	Q	C	L	K	E	Q	40
S	C	S	T	K	Y	R	T	L	R	Q	C	V	A	G	K	E	T	N	F	60
S	L	A	S	G	L	E	A	K	D	E	C	R	S	A	M	E	A	L	K	80
Q	K	S	L	Y	N	C	R	C	K	R	G	M	K	K	E	K	N	C	L	100
R	I	Y	W	S	M	Y	Q	S	L	Q	G	N	D	L	L	E	D	S	P	120
Y	E	P	V	N	S	R	L	S	D	I	F	R	V	V	P	F	I	S	D	140
V	F	Q	Q	V	E	H	I	P	K	G	N	N	C	L	D	A	A	K	A	160
C	N	L	D	D	I	C	K	K	Y	R	S	A	Y	I	T	P	C	T	T	180
S	V	S	N	D	V	C	N	R	R	K	C	H	K	A	L	R	Q	F	F	200
D	K	V	P	A	K	H	S	Y	G	M	L	F	C	S	C	R	D	I	A	220

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FIG. 2B

[illegible]

FIG.3A

Rat Glial Cell Line-Derived
Neurotrophic Factor Receptor Protein

10 30 50
AGCTCGCTCTCCCGGGCAGTGGTGTGGATGCACCGGAGTTCGGGGCGCTGGGCAAGTTGG

70 90 110
GTCGGAAC TGAACCCCTGAAAGCGGGTCCGCCCTCCCGCCCTCGCGCCCGCGGATCTGA

130 150 170
GTCGCTGGCGCGGTGGCGGCAGAGCGAGGGGAGTCTGCTCTCACCCCTGGATGGAGCT

FIG.3B

190 210 230
GAACTTTGAGTGGCCAGAGAGCGCAGTCGCCCGGGGATCGCTGCACGCTGAGCTCTCTC

250 270 290
CCCGAGACCGGCGCGGCTTTGGATTTTGGGGGGCGGGACGCTGCCGCGGGCAC

310 330 350
CATGTTCCTAGCCACTCTGTACTTCGCGCTGCCACTCCTGGATTTGCTGATGTCGCCCGA
M F L A T L Y F A L P L L D L L M S A E

370 390 410
GGTGAGTGGTGAGACCGCTGTGACTGTGTGAAAGCCAGCGATCAGTGCCCTGAAGGAACA
V S G G D R L D C V K A S D Q C L K E Q

FIG.3C

430 450 470
GAGCTGCAGCACCAAGTACCGCACACTAAGGCAGTGCGTGGCGGCAAGGAAACCAACTT
S C S T K Y R T L R Q C V A G K E T N F

490 510 530
CAGCCTGACATCCGGCCCTTGAGGCCCAAGGATGAGTGCCGTAGCGCCATGAGGCCCTTGAA
S L T S G L E A K D E C R S A M E A L K

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FIG.3D

550 570 590
GCAGAAGTCTCTGTACAACCTGCCGCTGCAAGCGGGGCATGAAGAAAGAGAAGAATTGTCT
Q K S L Y N C R C K R G M K K E K N C L

610 630 650
GCGTATCTACTGGAGCATGTACCAGAGCCCTGCAGGGAAATGACCTCCTGGGAAGATTCCCC
R I Y W S M Y Q S L Q G N D L L E D S P

670 690 710
GTATGAGCCGGTTAACAGCAGGTTGTCAGATATATCCGGGCAGTCCC GTTCATATCAGA
Y E P V N S R L S D I F R A V P F I S D

FIG.3E

730 750 770
TGT'TTCCAGCAAGTGGAAACACATTTCCAAAGGGAACAACCTGCCCTGGACGCAGCCCAAGGC
V F Q Q V E H I S K G N N C L D A A K A
790 810 830
CTGCAACCTGGACGACACCTGTAAAGTACAGGTCGGCCTACATCACCCCTGCACCAC
C N L D D T C K K Y R S A Y I T P C T T
850 870 890
CAGCATGTCCAACGAGGTCTGCAACCGCCGTAAGTGCCACAAGGCCCTCAGGCAGTTCTT
S M S N E V C N R R K C H K A L R Q F F

FIG.3F

910 930 950
CGACAAGGTTCCGGCCAAGCACAGCTACGGGATGCTCTTCTGCTCCTGCCGGGACATCGC
D K V P A K H S Y G M L F C S C R D I A

970 990 1010
CTGCACCGAGCGGGCGACAGACTATCGTCCCCGTGTGCTCCTATGAAGAACGAGAGAG
C T E R R R Q T I V P V C S Y E E R E R

1030 1050 1070
GCCCAACTGCCTGAGTCTGCAAGACTCCTGCAAGACCAATTACATCTGCAGATCTCGCCT
P N C L S L Q D S C K T N Y I C R S R L

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FIG.3G

1090	1110	1130
TGCAGATTTT	TACCAACTGCCAGCCAGAGTCAAGGTCTGTCAGCAACTGTCTTAAGGA	
A D F F T N C Q P E S R S V S N C L K E		
1150	1170	1190
GAACTACGCAGACTGCCCTCCTGGCCTACTCGGGACTGATTGGCACAGTCATGACTCCCAA		
N Y A D C L L A Y S G L I G T V M T P N		
1210	1230	1250
CTACGTAGACTCCAGCAGCCTCAGCGTGGCACCATGGTGTGACTGCAGCAACAGCGGCAA		
Y V D S S S L S V A P W C D C S N S G N		

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FIG.3H

1270	1290	1310
TGACCTGGAAGACTGCTTGAAATTTCTGAATTTTTTAAGGACAATACTTGCTCTCAAAA		
D L E D C L K F L N F F K D N T C L K N		
1330	1350	1370
TGCAATTCAAGCCTTTGGCAATGGCTCAGATGTGACCATGTGGCAGCCAGCCCTCCAGT		
A I Q A F G N G S D V T M W Q P A P P V		
1390	1410	1430
CCAGACCACCACTGCCACCACCTACCACCTGCCCTTCCGGGTCAAGAACAAGCCCTCTGGGGCC		
Q T T T A T T T A F R V K N K P L G P		

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FIG.3I

1450	1470	1490
AGCAGGGTCTGAGAA	TGAGATCCCACACAC	ACGTTTACCACCCCTGTGCGAA
A G S E N E I P T H V L P P C A N L Q A		TTTGCAGGC
1510	1530	1550
TCAGAAGCTGAAATCCA	ATGTGTCGGGTAGCACAC	ACCTCTGTCTTCTGATAGTATTT
Q K L K S N V S G S T H L C L S D S D F		
1570	1590	1610
CGGAAAGGATGGTCTCG	CTGGTGCCCTCCAGCCACATA	ACCACAAAATCAATGGCTGCTCC
G K D G L A G A S S H I T T K S M A A P		

FIG.3J

1630 1650 1670
TCCCAGCTGCAGTCTGAGCTCACTGCCGGTGCTGATGCTCACCGCCCTTGCTGCCCTGTT
P S C S L S S L P V L M L T A L A L L
1690 1710 1730
ATCTGTATCGTTGGCAGAAACGTCGTAGCTGCATCCGGGAAAACAGTATGAAAAGACAAA
S V S L A E T S *
1750 1770 1790
AGAGAACCAAGTATTCTGTCCCTGTCCCTCTTGTAATATCTGAAAATCCAGTTTAAAGCT
1810 1830 1850
CCGTTGAGAAGCAGTTTCACCCCAACTGGAACCTTTCCTTGTGTTTAAAGAAAGCTTGTTG

FIG.3K

1870 1890 1910
CCCTCAGGGGCTTCTGTTGAAGAACTGCTACAGGGGCTAATTCCAAACCCATAAGGCTCTG

1930 1950 1970
GGGCGTGTCGGGCTTAAGGGGACCATTTCACCATGTAAAGCAAGCTGGGCTTATCATG

1990 2010 2030
TGTTTGATGGTGAGGATGGTAGTGGTGATGATGATGGTAATTTAAACAGCTTGAACCCCTG

2050 2070 2090
TTCCTCTACTGGTTAGGAACAGGAGATACTATTGATAAAGATTCTTCCATGCTTACTC

2110 2130
AGCAGCATTCCTTCTGAAGACAGGCCCGCAGCCGTCG

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FIG.4A

Rat Glial Cell Line-Derived
Neurotrophic Factor Receptor Protein

M	F	L	A	T	L	Y	F	A	L	P	L	L	D	L	L	M	S	A	E	20
V	S	G	G	D	R	L	D	C	V	K	A	S	D	Q	C	L	K	E	Q	40
S	C	S	T	K	Y	R	T	L	R	Q	C	V	A	G	K	E	T	N	F	60
S	L	T	S	G	L	E	A	K	D	E	C	R	S	A	M	E	A	L	K	80
Q	K	S	L	Y	N	C	R	C	K	R	G	M	K	K	E	K	N	C	L	100
R	I	Y	W	S	M	Y	Q	S	L	Q	G	N	D	L	L	E	D	S	P	120
Y	E	P	V	N	S	R	L	S	D	I	F	R	A	V	P	F	I	S	D	140
V	F	Q	Q	V	E	H	I	S	K	G	N	N	C	L	D	A	A	K	A	160
C	N	L	D	D	T	C	K	K	Y	R	S	A	Y	I	T	P	C	T	T	180
S	M	S	N	E	V	C	N	R	R	K	C	H	K	A	L	R	Q	F	F	200
D	K	V	P	A	K	H	S	Y	G	M	L	F	C	S	C	R	D	I	A	220
C	T	E	R	R	R	Q	T	I	V	P	V	C	S	Y	E	E	R	E	R	240

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FIG.4B

P	N	C	L	S	L	Q	D	S	C	K	T	N	Y	I	C	R	S	R	L	260
A	D	F	F	T	N	C	Q	P	E	S	R	S	V	S	N	C	L	K	E	280
N	Y	A	D	C	L	L	A	Y	S	G	L	I	G	T	V	M	T	P	N	300
Y	V	D	S	S	S	L	S	V	A	P	W	C	D	C	S	N	S	G	N	320
D	L	E	D	C	L	K	F	L	N	F	F	K	D	N	T	C	L	K	N	340
A	I	Q	A	F	G	N	G	S	D	V	T	M	W	Q	P	A	P	P	V	360
Q	T	T	A	T	T	T	T	T	A	F	R	V	K	N	K	P	L	G	P	380
A	G	S	E	N	E	I	P	T	H	V	L	P	P	C	A	N	L	Q	A	400
Q	K	L	K	S	N	V	S	G	S	T	H	L	C	L	S	D	S	D	F	420
G	K	D	G	L	A	G	A	S	S	H	I	T	T	K	S	M	A	A	P	440
P	S	C	S	L	S	S	L	P	V	L	M	L	T	A	L	A	A	L	L	460
S	V	S	L	A	E	T	S	*												

468

FIG.5A

Human GDNF receptor Clones -- Alignment to generate

consensus sequence

-237

-188

Gdnfr	AATCTGGCCT	CGGAACACGC	CATTCTCCGC	GCCGCTTCCA	ATAACCACTA
Hsgr-21af	TCTGGCCT	CGGAACACGC	CATTCTCCGC	GCCGCTTCCA	ATAACCACTA
Hsgr-21bf	AATCTGGCCT	CGGAACACGC	CATTCTCCGC	GCCGCTTCCA	ATAACCACTA
21acon	TCTGGCCT	CGGAACACGC	CATTCTCCGC	GCCGCTTCCA	ATAACCACTA
21bcon	AATCTGGCCT	CGGAACACGC	CATTCTCCGC	GCCGCTTCCA	ATAACCACTA

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-187

-138

Gdnfr	ACATCCCCTAA	CGAGCATCCG	AGCCGAGGGC	TCTGCTCGGA	AATCGTCCTG
Hsgr-21af	ACATCCCCTAA	CGAGCATCCG	AGCCGAGGGC	TCTGCTCGGA	AATCGTCCTG
Hsgr-21bf	ACATCCCCTAA	CGAGCATCCG	AGCCGAGGGC	TCTGCTCGGA	AATCGTCCTG
21acon	ACATCCCCTAA	CGAGCATCCG	AGCCGAGGGC	TCTGCTCGGA	AATCGTCCTG
21bcon	ACATCCCCTAA	CGAGCATCCG	AGCCGAGGGC	TCTGCTCGGA	AATCGTCCTG

3 0 / 1 3 5

FIG.5B

-137	-88
Gdnfr	GCCCAACTCG GCCCTTCGAG CTCCTGAAGA TTACCGCATC TATTTTTTTT
Hsgr-21af	GCCCAACTCG GCCCTTCGAG CTCCTGAAGA TTACCGCATC TATTTTTTTT
Hsgr-21bf	GCCCAACTCG GCCCTTCGAG CTCCTGAAGA TTACCGCATC TATTTTTTTT
21acon	GCCCAACTCG GCCCTTCGAG CTCCTGAAGA TTACCGCATC TATTTTTTTT
21bcon	GCCCAACTCG GCCCTTCGAG CTCCTGAAGA TTACCGCATC TATTTTTTTT
-87	-38
Gdnfr	TTCTTTTTTTT TCTTTTCCCTA GCGCAGATAA AGTGAGCCCG GAAAGGGAAG
Hsgr-21af	TTCTTTTTTTT TCTTTTCCCTA GCGCAGATAA AGTGAGCCCG GAAAGGGAAG
Hsgr-21bf	TTCTTTTTTTT TCTTTTCCCTA GCGCAGATAA AGTGAGCCCG GAAAGGGAAG
21acon	TTCTTTTTTTT TCTTTTCCCTA GCGCAGATAA AGTGAGCCCG GAAAGGGAAG
21bcon	TTCTTTTTTTT TCTTTTCCCTA GCGCAGATAA AGTGAGCCCG GAAAGGGAAG

FIG. 5C

12

- 37

Gdnfr GAGGGGGCGG GGACACCATT GCCCTGAAAG AATAAATAAG TAAATAAACA
Hsgr - 21af GAGGGGGCGG GGACACCATT GCCCTGAAAG AATAAATAAG TAAATAAACA
Hsgr - 21bf GAGGGGGCGG GGACACCATT GCCCTGAAAG AATAAATAAG TAAATAAACA
21acon GAGGGGGCGG GGACACCATT GCCCTGAAAG AATAAATAAG TAAATAAACA
21bcon GAGGGGGCGG GGACACCATT GCCCTGAAAG AATAAATAAG TAAATAAACA

3 1 / 1 3 5

62

13

Gdnfr AACTGGCTCC TCGCCGCAGC TGGACGCCGT CGGTTGAGTC CAGGTTGGGT
Hsgr - 21af AACTGGCTCC TCGCCGCAGC TGGACGCCGT CGGTTGAGTC CAGGTTGGGT
Hsgr - 21bf AACTGGCTCC TCGCCGCAGC TGGACGCCGT CGGTTGAGTC CAGGTTGGGT
21acon AACTGGCTCC TCGCCGCAGC TGGACGCCGT CGGTTGAGTC CAGGTTGGGT
21bcon AACTGGCTCC TCGCCGCAGC TGGACGCCGT CGGTTGAGTC CAGGTTGGGT

3 2 / 1 3 5

FIG. 5D

63		112
	Gdnfr	CGGACCTGAA CCCCTAAAAG CGGAACCGCC TCCCGCCCTC GCCATCCCCG
	Hsgr-21af	CGGACCTGAA CCCCTAAAAG CGGAACCGCC TCCCGCCCTC GCCATCCCCG
	Hsgr-21bf	CGGACCTGAA CCCCTAAAAG CGGAACCGCC TCCCGCCCTC GCCATCCCCG
	21acon	CGGACCTGAA CCCCTAAAAG CGGAACCGCC TCCCGCCCTC GCCATCCCCG
	21bcon	CGGACCTGAA CCCCTAAAAG CGGAACCGCC TCCCGCCCTC GCCATCCCCG
113		162
	Gdnfr	AGCTGAGTCG CCGGCGGCGG TGGCTGCTGC CAGACCCGGA GTTTCCTCTT
	Hsgr-21af	AGCTGAGTCG CCGGCGGCGG TGGCTGCTGC CAGACCCGGA GTTTCCTCTT
	Hsgr-21bf	AGCTGAGTCG CCGGCGGCGG TGGCTGCTGC CAGACCCGGA GTTTCCTCTT
	21acon	AGCTGAGTCG CCGGCGGCGG TGGCTGCTGC CAGACCCGGA GTTTCCTCTT
	21bcon	AGCTGAGTCG CCGGCGGCGG TGGCTGCTGC CAGACCCGGA GTTTCCTCTT

3 3 / 1 3 5

FIG.5E

	163		212
Gdnfr	TCACTGGATG	GAGCTGAACT	TTGGGCGGCC AGAGCAGCAC AGCTGTCCGG
Hsgr-21af	TCACTGGATG	GAGCTGAACT	TTGGGCGGCC AGAGCAGCAC AGCTGTCCGG
Hsgr-21bf	TCACTGGATG	GAGCTGAACT	TTGGGCGGCC AGAGCAGCAC AGCTGTCCGG
21acon	TCACTGGATG	GAGCTGAACT	TTGGGCGGCC AGAGCAGCAC AGCTGTCCGG
21bcon	TCACTGGATG	GAGCTGAACT	TTGGGCGGCC AGAGCAGCAC AGCTGTCCGG

FIG.5F

	213		262
Gdnfr	GGATCGCTGC	ACGCTGAGCT	CCCTCGGCAA GACCCAGCGG CGGCTCGGGA
Hsgr-21af	GGATCGCTGC	ACGCTGAGCT	CCCTCGGCAA GACCCAGCGG CGGCTCGGGA
Hsgr-21bf	GGATCGCTGC	ACGCTGAGCT	CCCTCGGCAA GACCCAGCGG CGGCTCGGGA
21acon	GGATCGCTGC	ACGCTGAGCT	CCCTCGGCAA GACCCAGCGG CGGCTCGGGA
21bcon	GGATCGCTGC	ACGCTGAGCT	CCCTCGGCAA GACCCAGCGG CGGCTCGGGA
	263		312
Gdnfr	TTTTTTTGGG	GGGGCGGGGA	CCAGCCCCCGC GCCGGCACCA TGTTCCCTGGC
Hsgr-21af	TTTTTTTGGG		
Hsgr-21bf	TTTTTTTGGG		
21acon	TTTTTTTGGG	GGGGCGGGGA	CCAGCCCCCGC GCCGGCACCA TGTTCCCTGGC
21bcon	TTTTTTTGGG	GGGGCGGGGA	CCAGCCCCCGC GCCGGCACCA TGTTCCCTGGC

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FIG. 5G

313
Gdnfr GACCCTGTAC TTCGGGCTGC CGCTCTTGGA CTTGCTCCTG TCGGCCGAAG 362
21acon GNCCCTGTAC TTCGGGCTGC CGCTCTTGGA CTTGCTCCTG TCGGCCGAAG
21bcon GACCCTGTAC TTCGGGCTGC CGCTCTTGGA CTTGCTCCTG TCGGCCGAAG

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363
Gdnfr TGAGCGGCGG AGACCGCCTG GATTGCGTGA AAGCCAGTGA TCAGTGCCTG 412
21acon TGAGCGGCGG AGACCGCCTG GATTGCGTGA AAGCCAGTGA TCAGTGCCTG
21bcon TGAGCGGCGG AGACCGCCTG GATTGCGTGA AAGCCAGTGA TCAGTGCCTG

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FIG. 5H

413	462
Gdnfr	AAGGAGCAGA GCTGCAGCAC CAAGTACCGC ACGCTAAGGC AGTGCGTGGC
21acon	AAGGAGCAGA GCTGCAGCAC CAAGTACCGC ACGCTAAGGC AGTGCGTGGC
21bcon	AAGGAGCAGA GCTGCAGCAC CAAGTACCGC ACGCTAAGGC AGTGCGTGGC
463	512
Gdnfr	GGGCAAGGAG ACCAACTTCA GCCTGGCATC CGGCCTGGAG GCCAAGGATG
21acon	GGGCAAGGAG ACCAACTTCA GCCTGGCATC CGGCCTGGAG GCCAAGGATG
21bcon	GGGCAAGGAG ACCAACTTCA GCCTGGCATC CGGCCTGGAG GCCAAGGATG

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FIG. 5I

513	562
Gdnfr	AGTGCCGCAG CGCCATGGAG GCCCTGAAGC AGAAGTCGCT CTACAACCTGC
21acon	AGTGCCGCAG CGCCATGGAG GCCCTGAAGC AGAAGTCGCT CTACAACCTGC
21bcon	AGTGCCGCAG CGCCATGGAG GCCCTGAAGC AGAAGTCGCT CTACAACCTGC
563	612
Gdnfr	CGCTGCAAGC GGGGTATGAA GAAGGAGAAG AACTGCCCTGC GCATTTACTG
21acon	CGCTGCAAGC GGGGTATGAA GAAGGAGAAG AACTGCCCTGC GCATTTACTG
21bcon	CGCTGCAAGC GGGGTATGAA GAAGGAGAAG AACTGCCCTGC GCATTTACTG
613	662
Gdnfr	GAGCATGTAC CAGAGCCTGC AGGGAAATGA TCTGCTGGAG GATTCCCCAT
21acon	GAGCATGTAC CAGAGCCTGC AGGGAAATGA TCTGCTGGAG GATTCCCCAT
21bcon	GAGCATGTAC CAGAGCCTGC AGGGAAATGA TCTGCTGGAG GATTCCCCAT

FIG. 5J

663 712
Gdnfr ATGAACCAGT TAACAGCAGA TTGTCAGATA TATCCGGGT GGTCCCATTC
21acon ATGAACCAGT TAACAGCAGA TTGTCAGATA TATCCGGGT GGTCCCATTC
21bcon ATGAACCAGT TAACAGCAGA TTGTCAGATA TATCCGGGT GGTCCCATTC

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713 762
Gdnfr ATATCAGATG TTTTTCAGCA AGTGGAGCAC ATTCCCAAAG GGAACAACCTG
21acon ATATCAGATG TTTTTCAGCA AGTGGAGCAC ATTCCCAAAG GGAACAACCTG
21bcon ATATCAGATG TTTTTCAGCA AGTGGAGCAC ATTCCCAAAG GGAACAACCTG

FIG. 5K

763 812

Gdnfr CCTGGATGCA GCGAAGGCCT GCAACCTCGA CGACATTGCG AAGAAGTACA

21acon CCTGGATGCA GCGAAGGCCT GCAACCTCGA CGACATTGCG AAGAAGTACA

21bcon CCTGGATGCA GCGAAGGCCT GCAACCTCGA CGACATTGCG AAGAAGTACA

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813 862

Gdnfr GGTGCGCGTA CATCACCCCG TGCACCACCA GCGTGTCCAA .GATGTCTGC

Hsgr - 29a GTCGCGCGTA CATCACCCCG TGCACCACCA GCGTGTCCAA TGATGTCTGC

21acon GGTGCGCGTA CATCACCCCG TGCACCACCA GCGTGTCCAA CGATGTCTGC

21bcon GGTGCGCGTA CATCACCCCG TGCACCACCA GCGTGTCCAA CGATGTCTGC

29brc GTCGCGCGTA CATCACCCCG TGCACCACCA GCGTGTCCAA TGATGTCTGC

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FIG. 5L

863	912
Gdnfr	AACCGCCGCA AGTGCCACAA GGCCTCCGG CAGTTCTTTG ACAAGGTCCC
Hsgr - 29a	AACCGCCGCA AGTGCCACAA GGCCTCCGG CAGTTCTTTG ACAAGGTCCC
21acon	AACCGCCGCA AGTGCCACAA GGCCTCCGG CAGTTCTTTG ACAAGGTCCC
21bcon	AACCGCCGCA AGTGCCACAA GGCCTCCGG CAGTTCTTTG ACAAGGTCCC
29brc	AACCGCCGCA AGTGCCACAA GGCCTCCGG CAGTTCTTTG ACAAGGTCCC
913	962
Gdnfr	GGCCAAGCAC AGTACGGAA TGCTCTTCTG CTCCTGCCGG GACATCGCCT
Hsgr - 29a	GGCCAAGCAC AGTACGGAA TGCTCTTCTG CTCCTGCCGG GACATCGCCT
21acon	GGCCAAGCAC AGTACGGAA TGCTCTTCTG CTCCTGCCGG GACATCGCCT
21bcon	GGCCAAGCAC AGTACGGAA TGCTCTTCTG CTCCTGCCGG GACATCGCCT
29brc	GGCCAAGCAC AGTACGGAA TGCTCTTCTG CTCCTGCCGG GACATCGCCT

FIG. 5M

963	1012
Gdnfr	GCACAGAGCG GAGGCGACAG ACCATCGTGC CTGTGTGCTC CTATGAAGAG
Hsgr-29a	GCACAGAGCG GAGGCGACAG ACCATCGTGC CTGTGTGCTC CTATGAAGAG
21acon	GCACAGAGCG GAGGCGACAG ACCATCGTGC CTGTGTGCTC CTATGAAGAG
21bcon	GCACAGAGCG GAGGCGACAG ACCATCGTGC CTGTGTGCTC CTATGAAGAG
29brc	GCACAGAGCG GAGGCGACAG ACCATCGTGC CTGTGTGCTC CTATGAAGAG
1013	1062
Gdnfr	AGGAGAGAAGC CCAACTGTTT GAATTTCAG GACTCCTGCA AGACGAATTA
Hsgr-21ar	GAATTTCAG GACTCCTGCA AGACGAATTA
Hsgr-21br	A
Hsgr-29a	AGGAGAGAAGC CCAACTGTTT GAATTTCAG GACTCCTGCA AGACGAATTA
21acon	AGGAGAGAAGC CCAACTGTTT GAATTTCAG GACTCCTGCA AGACGAATTA
21bcon	AGGAGAGAAGC CCAACTGTTT GAATTTCAG GACTCCTGCA AGACGAATTA
29brc	AGGAGAGAAGC CCAACTGTTT GAATTTCAG GACTCCTGCA AGACGAATTA

FIG. 5N

	1063		1112
Gdnfr	CATCTGCAGA TCTCGCCTTG CGGATTTTTT TACCAACTGC CAGCCAGAGT		
Hsgr-21ar	CATCTGCAGA TCTCGCCTTG CGGATTTTTT TACCAACTGC CAGCCAGAGT		
Hsgr-21br	CATCTGCAGA TCTCGCCTTG CGGATTTTTT TACCAACTGC CAGCCAGAGT		
Hsgr-29a	CATCTGCAGA TCTCGCCTTG CGGATTTTTT TACCAACTGC CAGCCAGAGT		
21acon	CATCTGCAGA TCTCGCCTTG CGGATTTTTT TACCAACTGC CAGCCAGAGT		
21bcon	CATCTGCAGA TCTCGCCTTG CGGATTTTTT TACCAACTGC CAGCCAGAGT		
29brc	CATCTGCAGA TCTCGCCTTG CGGATTTTTT TACCAACTGC CAGCCAGAGT	4 2 / 1 3 5	1162
	1113		
Gdnfr	CAAGGTCTGT CAGCAGCTGT CTAAAGGAAA ACTACGCTGA CTGCCCTCCTC		
Hsgr-21ar	CAAGGTCTGT CAGCAGCTGT CTAAAGGAAA ACTACGCTGA CTGCCCTCCTC		
Hsgr-21br	CAAGGTCTGT CAGCAGCTGT CTAAAGGAAA ACTACGCTGA CTGCCCTCCTC		
Hsgr-29a	CAAGGTCTGT CAGCAGCTGT CTAAAGGAAA ACTACGCTGA CTGCCCTCCTC		
21acon	CAAGGTCTGT CAGCAGCTGT CTAAAGGAAA ACTACGCTGA CTGCCCTCCTC		
21bcon	CAAGGTCTGT CAGCAGCTGT CTAAAGGAAA ACTACGCTGA CTGCCCTCCTC		
29brc	CAAGGTCTGT CAGCAGCTGT CTAAAGGAAA ACTACGCTGA CTGCCCTCCTC		

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FIG.50

	1163		1212
Gdnfr	GCCTACTCGG	GGCTTATTGG	CACAGTCATG ACCCCCAACT ACATAGACTC
Hsgr-21ar	GCCTACTCGG	GGCTTATTGG	CACAGTCATG ACCCCCAACT ACATAGACTC
Hsgr-21br	GCCTACTCGG	GGCTTATTGG	CACAGTCATG ACCCCCAACT ACATAGACTC
Hsgr-29a	GCCTACTCGG	GGCTTATTGG	CACAGTCATG ACCCCCAACT ACATAGACTC
21acon	GCCTACTCGG	GGCTTATTGG	CACAGTCATG ACCCCCAACT ACATAGACTC
21bcon	GCCTACTCGG	GGCTTATTGG	CACAGTCATG ACCCCCAACT ACATAGACTC
29brc	GCCTACTCGG	GGCTTATTGG	CACAGTCATG ACCCCCAACT ACATAGACTC

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FIG. 5P

	1213		1262
Gdnfr	CAGTAGCCCTC	AGTGTGGCCC	CATGGTGTGA CTGCAGCAAC AGTGGGAACG
Hsgr - 2			TGGGAACG
Hsgr - 21ar	CAGTAGCCCTC	AGTGTGGCCC	CATGGTGTGA CTGCAGCAAC AGTGGGAACG
Hsgr - 21br	CAGTAGCCCTC	AGTGTGGCCC	CATGGTGTGA CTGCAGCAAC AGTGGGAACG
Hsgr - 29a	CAGTAGCCCTC	AGTGTGGCCC	CATGGTGTGA CTGCAGCAAC AGTGGGAACG
21acon	CAGTAGCCCTC	AGTGTGGCCC	CATGGTGTGA CTGCAGCAAC AGTGGGAACG
21bcon	CAGTAGCCCTC	AGTGTGGCCC	CATGGTGTGA CTGCAGCAAC AGTGGGAACG
29brc	CAGTAGCCCTC	AGTGTGGCCC	CATGGTGTGA CTGCAGCAAC AGTGGGAACG

FIG.5Q

	1263				1312
Gdnfr	ACCTAGAAGA	GTGCTTGAAA	TTTTTTGAATT	TCTTCAAGGA	CAATACATGT
Hsgr - 2	ACCTAGAAGA	GTGCTTGAAA	TTTTTTGAATT	TCTTCAAGGA	CAATACATGT
Hsgr - 9	A	GTGCTTGAAA	TTTTTTGAATT	TCTTCAAGGA	CAATACATGT
Hsgr - 21ar	ACCTAGAAGA	GTGCTTGAAA	TTTTTTGAATT	TCTTCAAGGA	CAATACATGT
Hsgr - 21br	ACCTAGAAGA	GTGCTTGAAA	TTTTTTGAATT	TCTTCAAGGA	CAATACATGT
Hsgr - 29a	ACCTAGAAGA	GTGCTTGAAA	TTTTTTGAATT	TCTTCAAGGA	CAATACATGT
21acon	ACCTAGAAGA	GTGCTTGAAA	TTTTTTGAATT	TCTTCAAGGA	CAATACATGT
21bcon	ACCTAGAAGA	GTGCTTGAAA	TTTTTTGAATT	TCTTCAAGGA	CAATACATGT
29brc	ACCTAGAAGA	GTGCTTGAAA	TTTTTTGAATT	TCTTCAAGGA	CAATACATGT

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FIG. 5R

1313 1362

Gdnfr CTTAAAAATG CAATTCAAGC CTTTGGCAAT GGCTCCGATG TGACCGTG TG

Hsgr-2 CTTAAAAATG CAATTCAAGC CTTTGGCAAT GGCTCCGATG TGACCGTG TG

Hsgr-9 CTTAAAAATG CAATTCAAGC CTTTGGCAAT GGCTCCGATG TGACCGTG TG

Hsgr-21ar CTTAAAAATG CAATTCAAGC CTTTGGCAAT GGCTCCGATG TGACCGTG TG

Hsgr-21br CTTAAAAATG CAATTCAAGC CTTTGGCAAT GGCTCCGATG TGACCGTG TG

Hsgr-29a CTTAAAAATG CAATTCAAGC CTTTGGCAAT GGCTCCGATG TGACCGTG TG

21acon CTTAAAAATG CAATTCAAGC CTTTGGCAAT GGCTCCGATG TGACCGTG TG

21bcon CTTAAAAATG CAATTCAAGC CTTTGGCAAT GGCTCCGATG TGACCGTG TG

29brc CTTAAAAATG CAATTCAAGC CTTTGGCAAT GGCTCCGATG TGACCGTG TG

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FIG. 5S

1363 1412

Gdnfr GCAGCCAGCC TTCCCAGTAC AGACCACCAC TGCCaCTACC ACCACTGCCCC

Hsgr-2 GCAGCCAGCC TTCCCAGTAC AGACCACCAC TGCCACTACC ACCACTGCCCC

Hsgr-9 GCAGCCAGCC TTCCCAGTAC AGACCACCAC TGCCACTACC ACCACTGCCCC

Hsgr-21ar GCAGCCAGCC TTCCCAGTAC AGACCACCAC TGCCACTACC ACCACTGCCCC

Hsgr-21br GCAGCCAGCC TTCCCAGTAC AGACCACCAC TGCCACTACC ACCACTGCCCC

Hsgr-29a GCAGCCAGCC TTCCCAGTAC AGACCACCAC TGCCGCTACC ACCACTGCCCC

21acon GCAGCCAGCC TTCCCAGTAC AGACCACCAC TGCCACTACC ACCACTGCCCC

21bcon GCAGCCAGCC TTCCCAGTAC AGACCACCAC TGCCACTACC ACCACTGCCCC

29brc GCAGCCAGCC TTCCCAGTAC AGACCACCAC TGCCGCTACC ACCACTGCCCC

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FIG. 5T

	1413		1462
Gdnfr	TCCGGGTAA	GAACAAGCCC	CTGGGGCCAG CAGGCTCTGA GAATGAAATT
Hsgr-2	TCCGGGTAA	GAACAAGCCC	CTGGGGCCAG CAGGCTCTGA GAATGAAATT
Hsgr-9	TCCGGGTAA	GAACAAGCCC	CTGGGGCCAG CAGGCTCTGA GAATGAAATT
Hsgr-21ar	TCCGGGTAA	GAACAAGCCC	CTGGGGCCAG CAGGCTCTGA GAATGAAATT
Hsgr-21br	TCCGGGTAA	GAACAAGCCC	CTGGGGCCAG CAGGCTCTGA GAATGAAATT
Hsgr-29a	TCCGGGTAA	GAACAAGCCC	CTGGGGCCAG CAGGCTCTGA GAATGAAATT
21acon	TCCGGGTAA	GAACAAGCCC	CTGGGGCCAG CAGGCTCTGA GAATGAAATT
21bcon	TCCGGGTAA	GAACAAGCCC	CTGGGGCCAG CAGGCTCTGA GAATGAAATT
29brc	TCCGGGTAA	GAACAAGCCC	CTGGGGCCAG CAGGCTCTGA GAATGAAATT

FIG. 5U

1463 1512

Gdnfr CCCACTCATG TTTTGCCACC GTGTGCAAAT TTACAGGCAC AGAAGCTGAA

Hsgr-2 CCCACTCATG TTTTGCCACC GTGTGCAAAT TTACAGGCAC AGAAGCTGAA

Hsgr-9 CCCACTCATG TTTTGCCACC GTGTGCAAAT TTACAGGCAC AGAAGCTGAA

Hsgr-21ar CCCACTCATG TTTTGCCACC GTGTGCAAAT TTACAGGCAC AGAAGCTGAA

Hsgr-21br CCCACTCATG TTTTGCCACC GTGTGCAAAT TTACAGGCAC AGAAGCTGAA

Hsgr-29a CCCACTCATG TTTTGCCACC GTGTGCAAAT TTACAGGCAC AGAAGCTGAA

21acon CCCACTCATG TTTTGCCACC GTGTGCAAAT TTACAGGCAC AGAAGCTGAA

21bcon CCCACTCATG TTTTGCCACC GTGTGCAAAT TTACAGGCAC AGAAGCTGAA

29brc CCCACTCATG TTTTGCCACC GTGTGCAAAT TTACAGGCAC AGAAGCTGAA

FIG.5V

	1513		1562
Gdnfr	ATCCAATGTG	TCGGGCAATA	CACACCTCTG TATTTCCAAT GGTAATTATG
Hsgr-2	ATCCAATGTG	TCGGGCAATA	CACACCTCTG TATTTCCAAT GGTAATTATG
Hsgr-9	ATCCAATGTG	TCGGGCAATA	CACACCTCTG TATTTCCAAT GGTAATTATG
Hsgr-21ar	ATCCAATGTG	TCGGGCAATA	CACACCTCTG TATTTCCAAT GGTAATTATG
Hsgr-21br	ATCCAATGTG	TCGGGCAATA	CACACCTCTG TATTTCCAAT GGTAATTATG
21acon	ATCCAATGTG	TCGGGCAATA	CACACCTCTG TATTTCCAAT GGTAATTATG
21bcon	ATCCAATGTG	TCGGGCAATA	CACACCTCTG TATTTCCAAT GGTAATTATG
29brc	ATCCAATGTG	TCGGGCAATA	CACACCTCTG TATTTCCAAT GGTAATTATG

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FIG. 5W

1563
1612

Gdnfr AAAAAGAAGG TCTCGGTGCT TCCAGCCACA TAACCCACAAA ATCAATGGCT
Hsgr-2 AAAAAGAAGG TCTCGGTGCT TCCAGCCACA TAACCCACAAA ATCAATGGCT
Hsgr-9 AAAAAGAAGG TCTCGGTGCT TCCAGCCACA TAACCCACAAA ATCAATGGCT
Hsgr-21ar AAAAAGAAGG TCTCGGTGCT TCCAGCCACA TAACCCACAAA ATCAATGGCT
Hsgr-21br AAAAAGAAGG TCTCGGTGCT TCCAGCCACA TAACCCACAAA ATCAATGGCT
21acon AAAAAGAAGG TCTCGGTGCT TCCAGCCACA TAACCCACAAA ATCAATGGCT
21bcon AAAAAGAAGG TCTCGGTGCT TCCAGCCACA TAACCCACAAA ATCAATGGCT
29brc AAAAAGAAGG TCTCGGTGCT TCCAGCCACA TAACCCACAAA ATCAATGGCT

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FIG.5X

	1613		1662
Gdnfr	GCTCCTCCAA	GCTGTGGTCT	GAGCCCACTG CTGGTCCTGG TGGTAACCGC
Hsgr - 2	GCTCCTCCAA	GCTGTGGTCT	GAGCCCACTG CTGGTCCTGG TGGTAACCGC
Hsgr - 9	GCTCCTCCAA	GCTGTGGTCT	GAGCCCACTG CTGGTCCTGG TGGTAACCGC
Hsgr - 21ar	GCTCCTCCAA	GCTGTGGTCT	GAGCCCACTG CTGGTCCTGG TGGTAACCGC
Hsgr - 21br	GCTCCTCCAA	GCTGTGGTCT	GAGCCCACTG CTGGTCCTGG TGGTAACCGC
21acon	GCTCCTCCAA	GCTGTGGTCT	GAGCCCACTG CTGGTCCTGG TGGTAACCGC
21bcon	GCTCCTCCAA	GCTGTGGTCT	GAGCCCACTG CTGGTCCTGG TGGTAACCGC
29brc	GCTCCTCCAA	GCTGTGGTCT	GAGCCCACTG CTGGTCCTGG TGGTAACCGC

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FIG.5Y

	1663		1712
Gdnfr	TCTGTCCACC	CTATTATCTT	TAACAGAAAC ATCATAGCTG CATTAATAAAA
Hsgr-2	TCTGTCCACC	CTATTATCTT	TAACAGAAAC ATCATAGCTG CATTAATAAAA
Hsgr-9	TCTGTCCACC	CTATTATCTT	TAACAGAAAC ATCATAGCTG CATTAATAAAA
Hsgr-21ar	TCTGTCCACC	CTATTATCTT	TAACAGAAA
Hsgr-21br	TCTGTCCACC	CTATTATCTT	TAACAGAAA
21acon	TCTGTCCACC	CTATTATCTT	TAACAGAAA
21bcon	TCTGTCCACC	CTATTATCTT	TAACAGAAA
29brc	TCTGTCCACC	CTATTATCTT	TAACAGAAAC ATCATAGCTG CATTAATAAAA
	1713		1762
Gdnfr	ATACAATATG	GACATGTAAA	AAGACAAAAA CCAAGTTATC TGTTTCCTGT
Hsgr-2	ATACAATATG	GACATGTAAA	AAGACAAAAA CCAAGTTATC TGTTTCCTGT
Hsgr-9	ATACAATATG	GACATGTAAA	AAGACAAAAA CCAAGTTATC TGTTTCCTGT
29brc	ATACAATATG	GACATGTAAA	AAGACAAAAA CCAAGTTATC TGTTTCCTGT

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FIG. 5Z

	1763		1812
Gdnfr	TCTCTTGTAT	AGCTGAAATT	CCAGTTTAGG AGCTCAGTTG AGAAACAGTT
Hsgr - 2	TCTCTTGTAT	AGCTGAAATT	CCAGTTTAGG AGCTCAGTTG AGAAACAGTT
Hsgr - 9	TCTCTTGTAT	AGCTGAAATT	CCAGTTTAGG AGCTCAGTTG AGAAACAGTT
29brc	TCTCTTGTAT	AGCTGAAATT	CCAGTTTAGG AGCTCAGTTG AGAAACAGTT
	1813		1862
Gdnfr	CCATTCAACT	GGAACATTTT	TTTTTTT.CC TTTTAAGAAA GCTTCTTG TG
Hsgr - 2	CCATTCAACT	GGAACATTTT	TTTTTTT.CC TTTTAAGAAA GCTTCTTG TG
Hsgr - 9	CCATTCAACT	GGAACATTTT	TTTTTTT.TCC TTTTAAGAAA GCTTCTTG TG
29brc	CCATTCAACT	GGAACATTTT	TTTTTTT.CC TTTTAAGAAA GCTTCTTG TG

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FIG.5A A

	1863		1912
Gdnfr	ATCCCTTCGGG	GCTTCTGTGA AAAACCTGAT	GCAGTGCTCC ATCCAAACTC
Hsgr - 2	ATCCCTTCGGG	GCTTCTGTGA AAAACCTGAT	GCAGTGCTCC ATCCAAACTC
Hsgr - 9	ATCCCTTCGGG	GCTTCTGTGA AAAACCTGAT	GCAGTGCTCC ATCCAAACTC
29brc	ATCCCTTCGGG	GCTTCTGTGA AAAACCTGAT	GCAGTGCTCC ATCCAAACTC
	1913		1962
Gdnfr	AGAAGGCCTTT	GGGATATGCT GTATTTTAAA	GGGACAGTTT GTAACTTGGG
Hsgr - 2	AGAAGGCCTTT	GGGATATGCT GTATTTTAAA	GGGACAGTTT GTAACTTGGG
Hsgr - 9	AGAAGGCCTTT	GGGATATGCT GTATTTTAAA	GGGACAGTTT GTAACTTGGG
29brc	AGAAGGCCTTT	GGGATATGCT GTATTTTAAA	GGGACAGTTT GTAACTTGGG

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FIG.5B B

	1963	2012
Gdnfr	CTGTAAAGCA AACTGGGGCT GTGTTTTCGA TGATGATGAT CATCATGATC	
Hsgr-2	CTGTAAAGCA AACTGGGGCT GTGTTTTCGA TGATGATGAT CATCATGATC	
Hsgr-9	CTGTAAAGCA AACTGGGGCT GTGTTTTCGA TGATGATGAT GATCATGATG	
29brc	CTGTAAAGCA AACTGGGGCT GTGTTTTCGA TGATGATGAT CATCATGATC	
	2013	2062
Gdnfr	ATGAT.....GATTTT
Hsgr-2	ATGAT.....GATTTT
Hsgr-9	ATGATCATCA TGATCATGAT GATGATCATC ATGATCATGA TGATGATTTT	
29brc	ATGAT.....GATTTT

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FIG.5C C

	2063		2112
Gdnfr	AACAGTTTTTA	CTTCTGGCCT	TTCCCTAGCTA GAGAAGGAGT TAAATATTTCT
Hsgr-2	AACAGTTTTTA	CTTCTGGCCT	TTCCCTAGCTA GAGAAGGAGT TAAATATTTCT
Hsgr-9	AACAGTTTTTA	CTTCTGGCCT	TTCCCTAGCTA GAGAAGGAGT TAAATATTTCT
29brc	AACAGTTTTTA	CTTCTGGCCT	TTCCCTAGCTA GAGAAGGAGT TAAATATTTCT
	2113		2162
Gdnfr	AAGGTAAGTC	CCATATCTCC	TTTAAATGACA TTGATTCTTA ATGATATAAAA
Hsgr-2	AAGGTAAGTC	CCATATCTCC	TTTAAATGACA TTGATTCTTA ATGATATAAAA
Hsgr-9	AAGGTAAGTC	CCATATCTCC	TTTAAATGACA TTGATTCTTA ATGATATAAAA
29brc	AAGGTAAGTC	CCATATCTCC	TTTAAATGACA TTGATTCTTA ATGATATAAAA

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FIG.5D D

	2163		2212		
Gdnfr	TTTCAGCCCTA	CATTGATGCC	AAGCTTTTTT	GCCACAAAGA	AGATTCTTAC
Hsgr - 2	TTTCAGCCCTA	CATTGATGCC	AAGCTTTTTT	GCCACAAAGA	AGATTCTTAC
Hsgr - 9	TTTCAGCCCTA	CATTGATGCC	AAGCTTTTTT	GCCACAAAGA	AGATTCTTAC
29brc	TTTCAGCCCTA	CATTGATGCC	AAGCTTTTTT	GCCACAAAGA	AGATTCTTAC
	2213		2262		
Gdnfr	CAAGAGTGGG	CTTTGTGGAA	ACAGCTGGTA	CTGATGTTCA	CCTTTATATA
Hsgr - 2	CAAGAGTGGG	CTTTGTGGAA	ACAGCTGGTA	CTGATGTTCA	CCTTTATATA
Hsgr - 9	CAAGAGTGGG	CTTTGTGGAA	ACAGCTGGTA	CTGATGTTCA	CCTTTATATA
29brc	CAAGAGTGGG	CTTTGTGGAA	ACAGCTGGTA	CTGATGTTCA	CCTTTATATA

FIG.5E E

2263 2312
Gdnfr TGTACTAGCA TTTTCCACGC TGATGTTTAT GTACTGTAAA CAGTTCTGCA
Hsgr-2 TGTACTAGCA TTTTCCACGC TGATGTTTAT GTACTGTAAA CAGTTCTGCA
Hsgr-9 TGTACTAGCA TTTTCCACGC TGATGTTTAT GTACTGTAAA CAGTTCTGCA
29brc TGTACTAGCA TTTTCCACGC TGATGTTTAT GTACTGTAAA CAGTTCTGCA

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2313 2362
Gdnfr CTCCTGTACA AAAGAAAAAA CACCTGTCAC ATCCAAATAT AGTATCTGTC
Hsgr-2 CTCCTGTACA AAAGAAAA
Hsgr-9 CTCCTGTACA AAAGAAAA
29brc CTCCTGTACA AAAGAAAAAA CACCTGTCAC ATCCAAATAT AGTATCTGTC

FIG.5F F

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2363
Gdnfr TTTTCGTCAA AATAGAGAGT GGGGAATGAG TGTGCCGATT CAATACCTCA 2412
29brc TTTTCGTCAA AATAGAGAGT GGGGAATGAG TGTGCCGATT CAATACCTCA

2413
Gdnfr ATCCCTGAAC GACACTCTCC TAATCCTAAG CCTTACCCTGA GTGAGAAGCC 2462
29brc ATCCCTGAAC GACACTCTCC TAATCCTAAG CCTTACCCTGA GTGAGAAGCC

2463
Gdnfr CTTTACCCTAA CAAAAGTCCA ATATAGCTGA AATGTCGCTC TAATACTCTT 2512
29brc CTTTACCCTAA CAAAAGTCCA ATATAGCTGA AATGTCGCTC TAATACTCTT

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FIG.5G G

2513	2562
Gdnfr TACACATATG AGGTTATATG TAGAAAAAAA TTTTACTACT AAATGATTTC	
29brc TACACATATG AGGTTATATG TAGAAAAAAA TTTTACTACT AAATGATTTC	
2563	2612
Gdnfr AACTATTGGC TTTCCTATATT TTGAAAGTAA TGATATTGTC TCATTTTITTT	
29brc AACTATTGGC TTTCCTATATT TTGAAAGTAA TGATATTGTC TCATTTTITTT	
2613	2662
Gdnfr ACTGATGGTT TAATACAAAA TACACAGAGC TTGTTTCCCC TCATAAGTAG	
29brc ACTGATGGTT TAATACAAAA TACACAGAGC TTGTTTCCCC TCATAAGTAG	

FIG. 5H H

2663	2712
Gdnfr	TGTTTCGCTCT GATATGAACT TCACAAATAC AGCTCATCAA AAGCAGACTC
29brc	TGTTTCGCTCT GATATGAACT TCACAAATAC AGCTCATCAA AAGCAGACTC
2713	2762
Gdnfr	TGAGAAAGCCT CGTGCTGTAG CAGAAAGTTC TGCATCATGT GACTGTGGAC
29brc	TGAGAAAGCCT CGTGCTGTAG CAGAAAGTTC TGCATCATGT GACTGTGGAC
2763	2812
Gdnfr	AGGCAGGAGG AAACAGAACA GACAAGCATT GTCTTTTGTG ATTGCTCGAA
29brc	AGGCAGGAGG AAACAGAACA GACAAGCATT GTCTTTTGTG ATTGCTCGAA

FIG. 5I I

2862

Gdnfr GTGCAAGCGT GCATACCTGT GGAGGGAAC TGGGCTGCT TGTAATGTT
29brc GTGCAAGCGT GCATACCTGT GGAGGGAAC TGGGCTGCT TGTAATGTT

2912

Gdnfr CTGCAGCATC TCTTGACACA CTTGTCATGA CACAATCCAG TACCTTGGTT
29brc CTGCAGCATC TCTTGACACA CTTGTCATGA CACAATCCAG TACCTTGGTT

6 3 / 1 3 5

2962

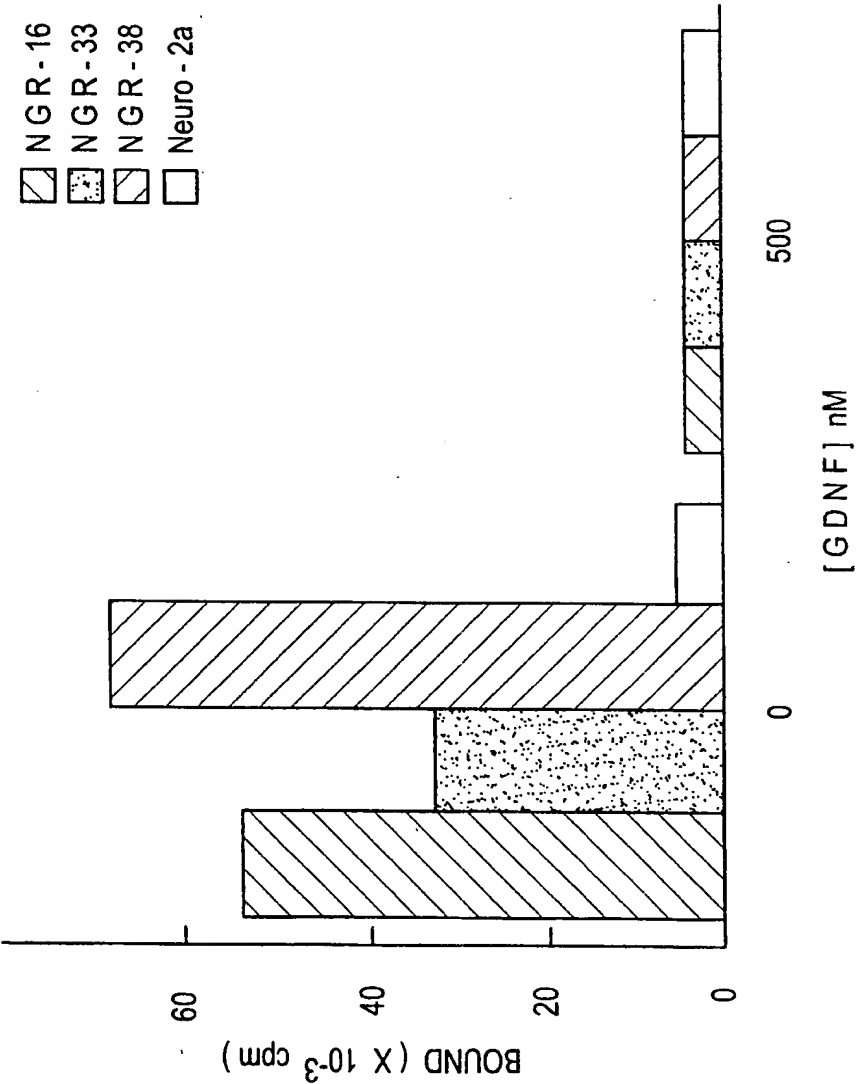
Gdnfr TTCAGGTTAT CTGACAAAGG CAGCTTTGAT TGGACATGG AGGCATGGGC
29brc TTCAGGTTAT CTGACAAAGG CAGCTTTGAT TGGACATGG AGGCATGGGC

2963

Gdnfr AGGCCGGAA
29brc AGGCCGGAA

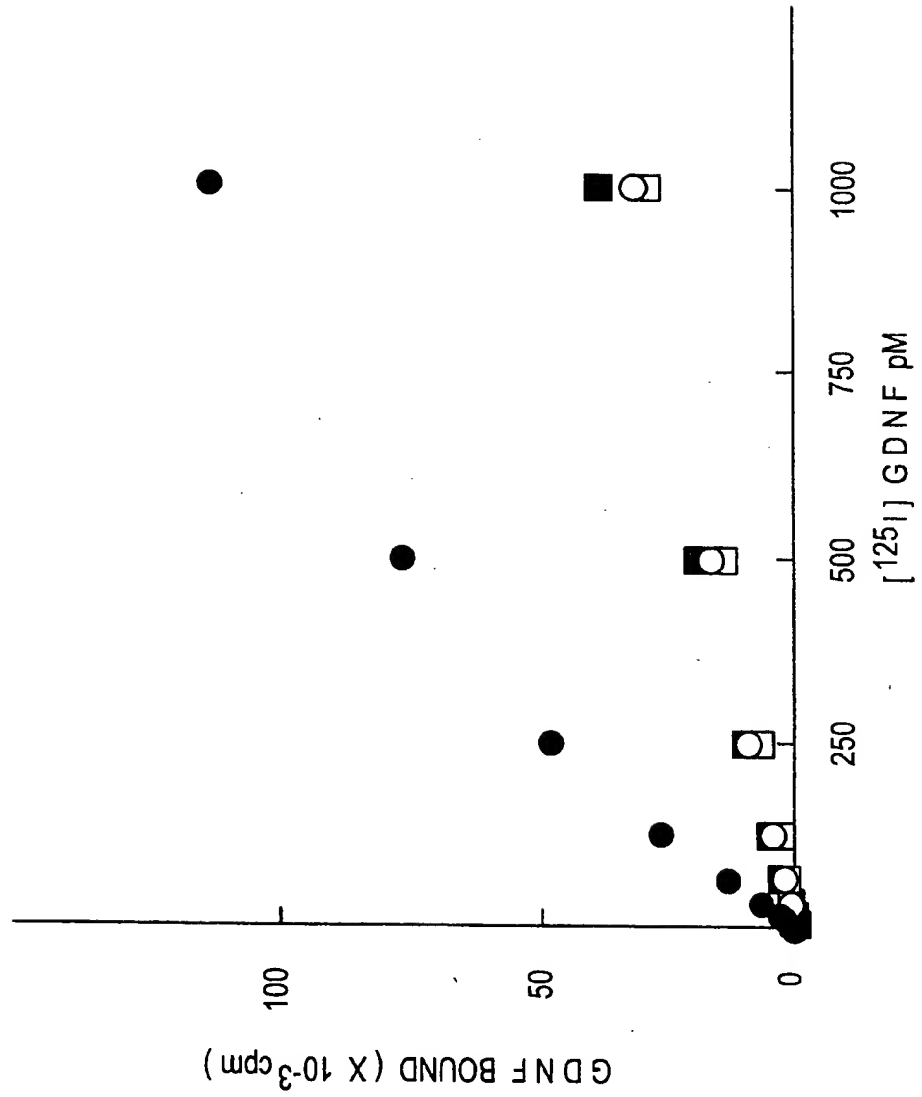
6 4 / 1 3 5

FIG. 6



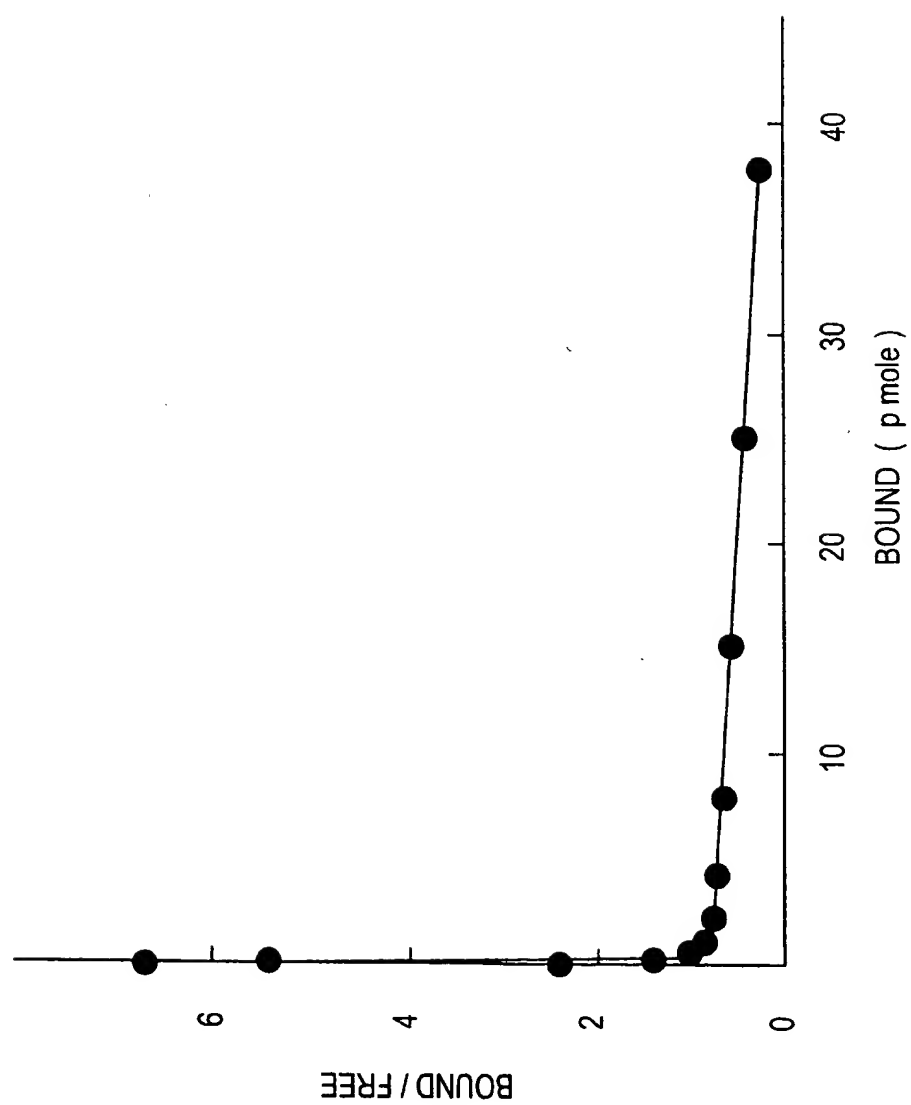
6 5 / 1 3 5

FIG. 7A



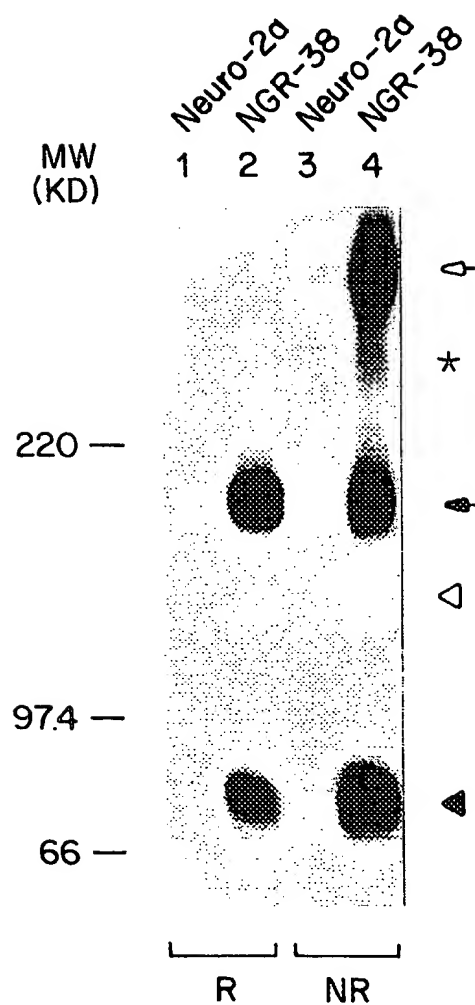
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FIG. 7B



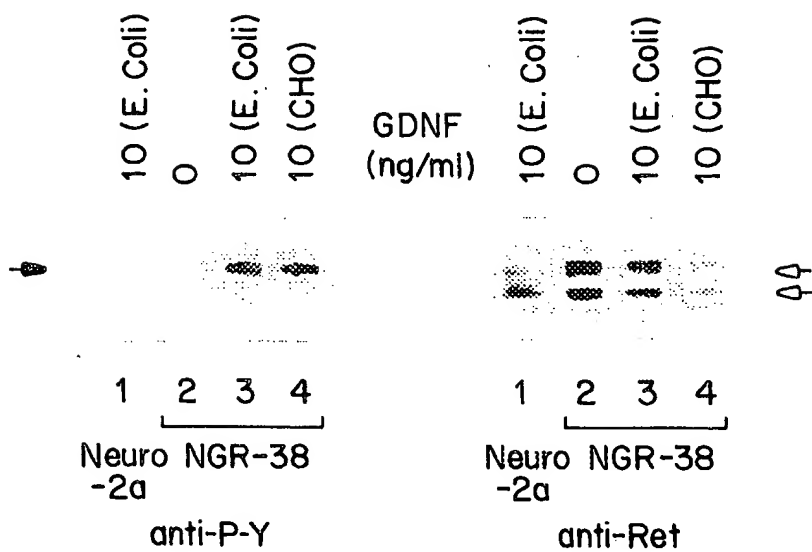
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FIG. 8



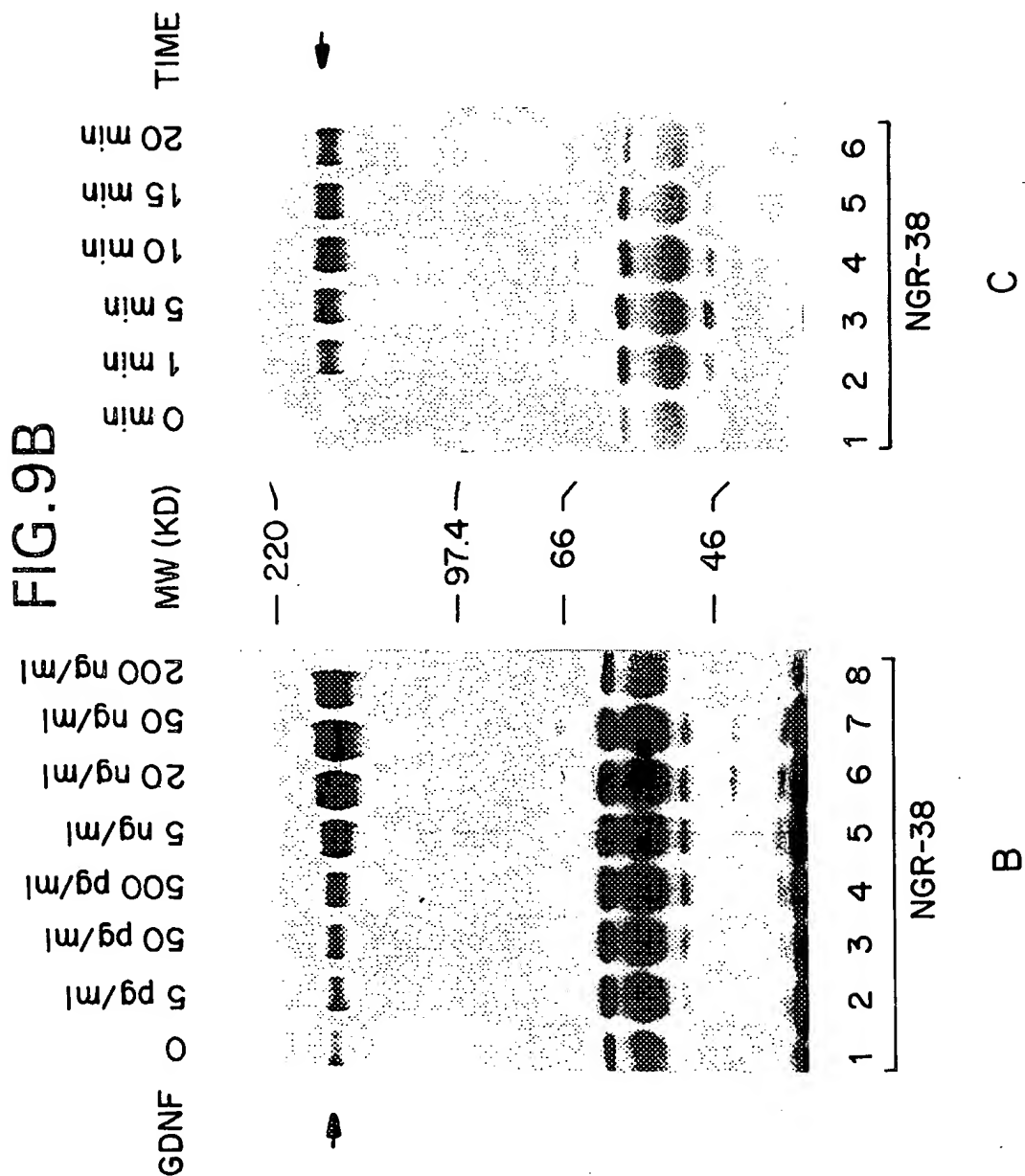
6 8 / 1 3 5

FIG.9A

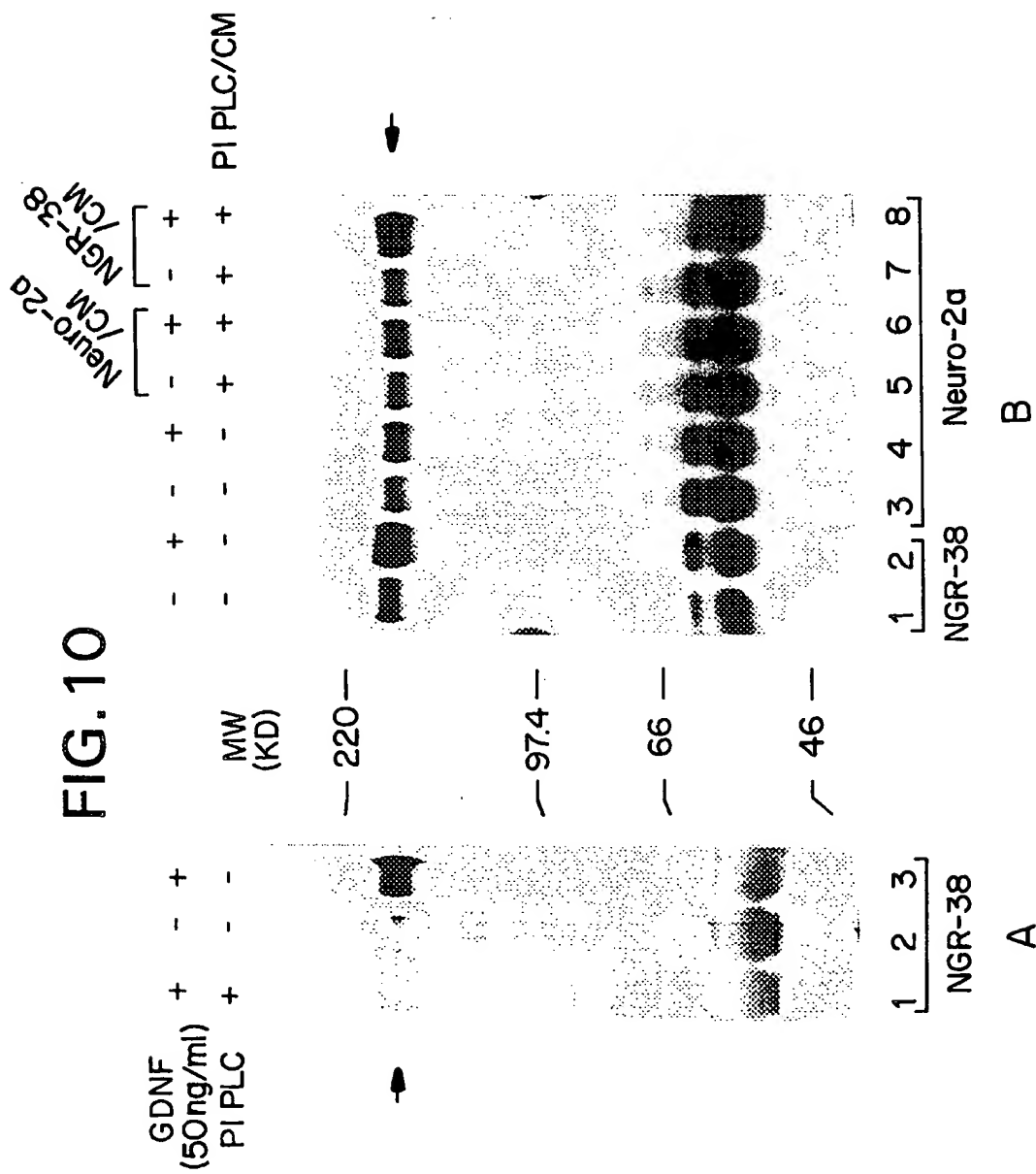


A

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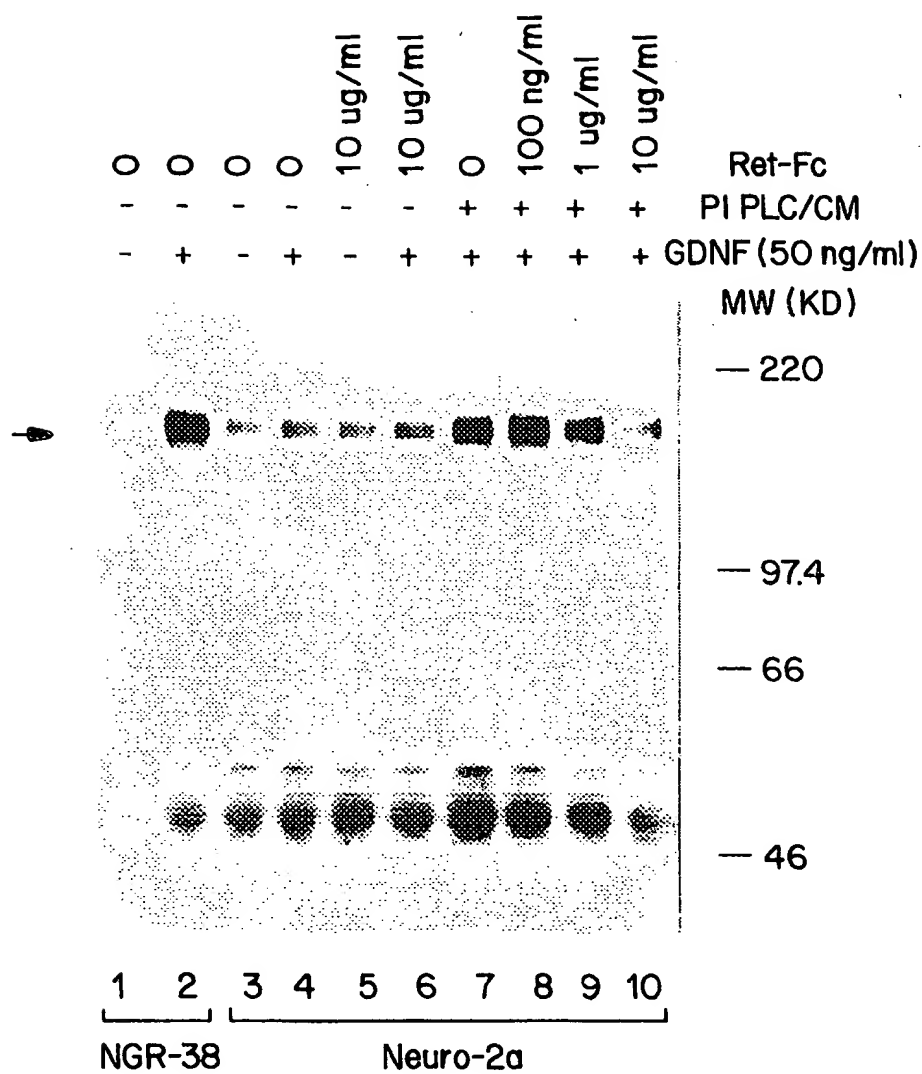


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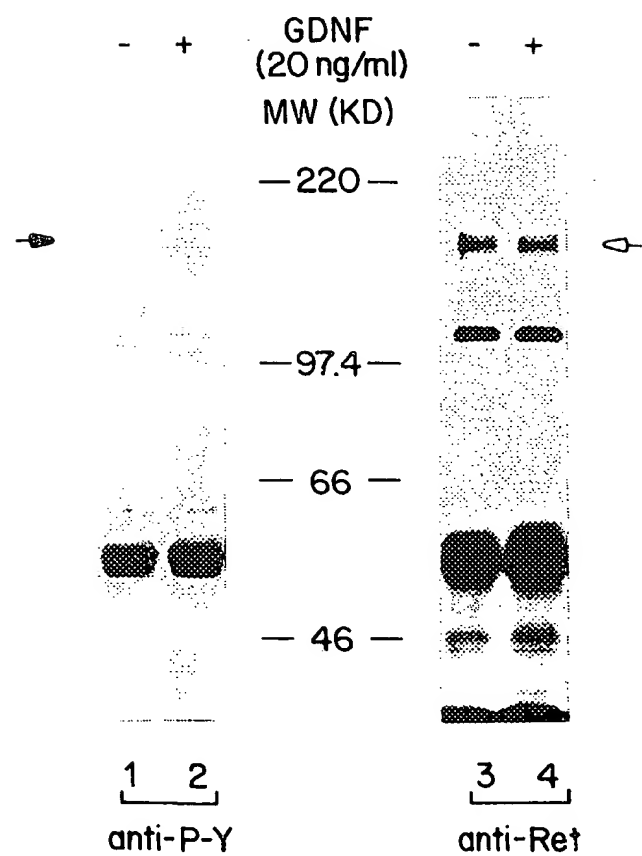
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FIG. 11



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FIG. 12



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FIG. 13

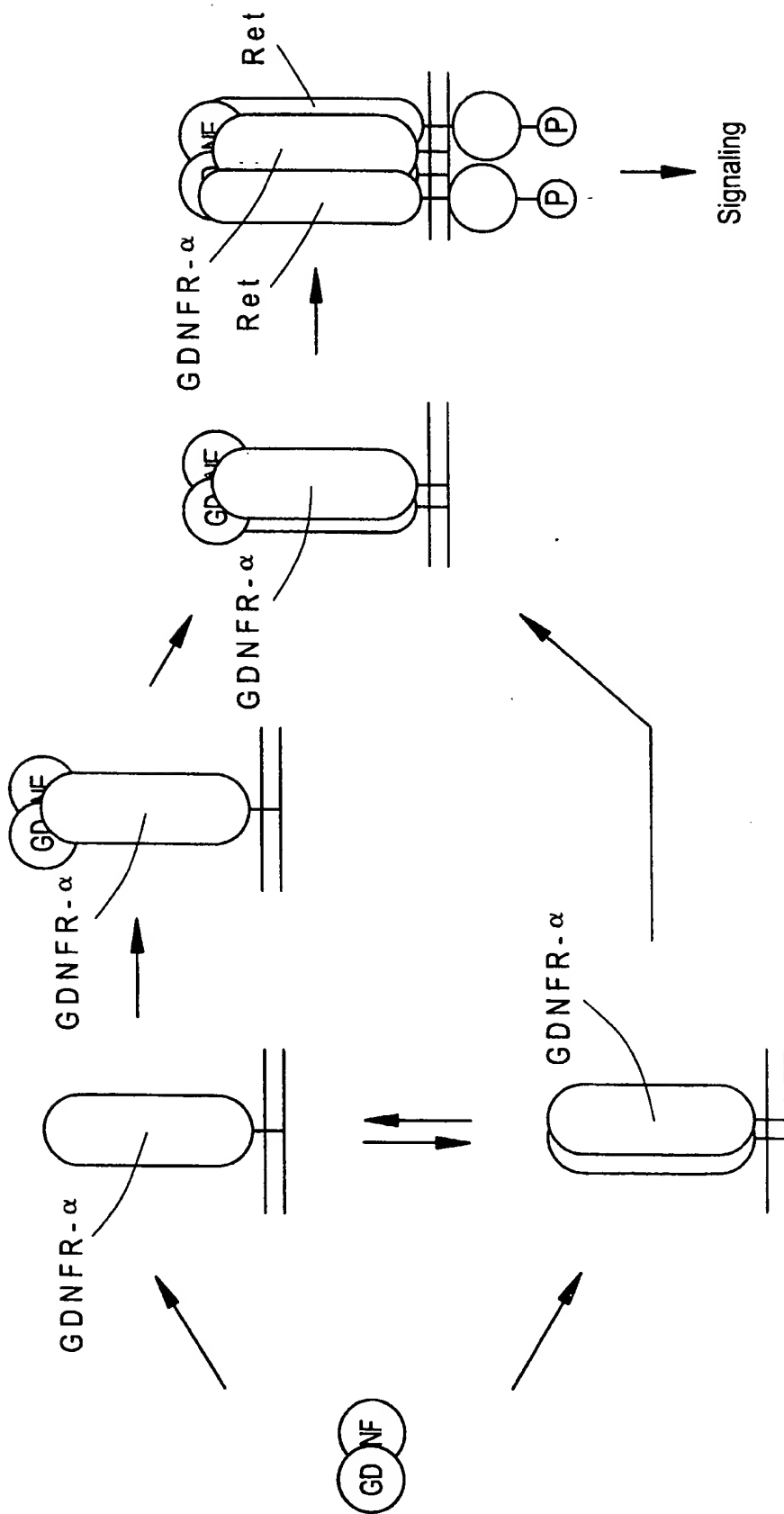


FIG. 14A

Human GRR2

1 CATGAAGAAACCTCAGTAAGTCTCAGACTTGGCCCCAAAGGAGCCCCAACTAGTTACTCCCT 60

61 GGTCGTACAGAGGATCTGGCTATTACACTCAACAGCAAAATTCATCAATCCCGCT 120

121 AAAGATATAAGAAATCACTAGGAAKAATAAGCCAGAACTCAAGACAGAAATAGCATTAAAGT 180

181 AGTTCCCTTCAGTACAGTGAGCAGAAAGCTGGCCCACTCTACGACTCTAWAAGACTCAGAAAA 240

241 GCTTACTAGGACCWCTGGGCATWCCGGTGTCCTATGTGGGATTCGTAACGCTTTGA 300

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360	GTGAGAGCTGCCCTCAAAATAGTTTCTTCTCAAAACGGTTTCAGGCTTTGTTAGAAAGG	360
361	GAAGACTTCACTGCCACTTTACCCAGATCATCTACCCCATCCTTGGAAATGAATGGGGAAG	420
421	CTTCAGCCACCCCTACCAGGCTCCTAAATCAACCACTTGAGAGAAAACTATAACGTTGC	480
481	TCTACAGTACTTCAGGAGGTTAAAGAAAGTCACAGAAAGAAAGAACTCTGGGAAACA	540
541	GTCAAATTCGGCTATTAAAGACATTAGTTACAGGCCCCCTGTACCTCTCCTAGAAACCCCT	600
601	GGGAGTACACCCGCAGAGAGAGAGAGCCCCAAGCCACCAAGCAAGTCAACCAATCTGGC	660
661	AAAGGGCGTCCCACCTGCGGCTTTCAGTCCAAGAAAGTGGATCCTGCTGTTCCGCAGTCTC	720

FIG. 14C

721 TCTTCTATCTCCTCACTTCCTATTTACCCCTTTGAAGTGGGTACTGAATAGCCCGTTCCCA 780
781 AGCAGAGGCCCTTTGTATACGGGGTGCTACAGTCGCCCTGGTGGAAACACCTTGGCAGAGT 840
841 TGTTTGGTGCCAGGATGGGCCCACTGAAGGCATCTGCTGTGGACACACACACACACA 900
901 CACACACACACACACACAGAGAGAGAGAGAGAAAGACACACGCCAGCAGAGACACAC 960
961 GGTCACGTGGAAATTCATTAGAAAAAAGTGAGCCGAGCAAGGGTTAGCGGAGAGATTTT 1020
1021 TTTGAATCTTGTCTTTCGTCTTGGTGCGAAAGAGCGACTCCAGTCTCTCGTCCCTCGAAGC 1080
1081 TCCGACTGGAATTGTTCTTGGGCGCTGACACCCGTCGTGGATTCTTTCTATTTCGATT 1140

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FIG.14D

1141 TTATCCGACCCCTCCCTCGCCGCTTCCTTCCAGCCCTTCACTCGCAAATCGCCCTCTCT 1200
1201 CCCCACCTCCCCAGGCCCTCCTGGGAAGCGCAGGGGAATTGGACCCCGGGGACTCACG 1260
1261 CCTTCCCGGACGATTGGAGGGGAGGGCTGACCCCAAGGACTGGGCTGTTGGCTTAGAAAGC 1320
1321 CGATACACAGATACGCGTATATTGATTGTAGCGGGCAAGGGGGCGTCGAGAGGCAGCA 1380
1381 GCCCATCGCCCGCTCTCACCCCAACCCCTCCAGCCAGAGCGGAGAAATCGCAGGACTCGG 1440
1441 GATCTTCATCGGGTGGACTAGCTGGGATCTCCGCATTGGATTGGGGCTGATTACCACTG 1500

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FIG.14E

1501 CTTGGCTATTATTATTGTTGTTGTTACTACTATTATTTTTTTTACCCAAGGAGAAAGA 1560

1561 CAAAAAACGGTGGGATTATTAAACATGATCTTGGCAACGTCCTTCTGCCCTCTTCTTCT 1620
1 M I L A N V F C L F F F

1621 TTCTAGACGACACCCCTCCGCTCTTTGGCCAGCCCTTCCCTCCCTGCAGGGCCCCGAGCTCC 1680
13 L D D T L R S L A S P S S L Q G P E L H 32 35

1681 ACGGCTGGCGCCCCCAGTGACTGTGTCCGGGGCCCAATGAGCTGTGTGCCCGCGAATCCA 1740
33 G W R P P V D C V R A N E L C A A E S N 52

1741 ACTGCAGCTCTCGCTACCGCACTCTGCGGCAGTGCCCTGGCAGCCGCGACCGCAACACCA 1800
53 C S S R Y R T L R Q C L A G R D R N T M 72

FIG. 14F

1801 TGCTGGCCAACAAGAGTGCCAGGCGCCTTGAGGTCTTGACGAGAGAGCCCGCTGTACG 1860
 73 L A N K E C Q A A L E V L Q E S P L Y D 92

1861 ACTGCCGCTGCAAGCGGGGCATGAAGAAGGAGCTGCAGTGTCTGCAGATCTACTGGAGCA 1920
 93 C R C K R G M K K E L Q C L Q I Y W S I 112

1921 TCCACCTGGGGCTGACCGAGGGTGAGGAGTTCTACGAAGCCTCCCCCTATGAGCCGGTGA 1980
 113 H L G L T E G E F Y E A S P Y E P V T 132

1981 CCTCCCGCCTCTCGGACATCTTCAGGCTTGCTTCAATCTTCTCAGGGACAGGGGCAGACC 2040
 133 S R L S D I F R L A S I F S G T G A D P 152

2041 CGGTGGTCAGCGCCAAAGAGCAACCATGCGCTGGATGCTGCCAAGGCGCTGCAACCTGAATG 2100
 153 V V S A K S N H C L D A A K A C N L N D 172

2101 ACAACTGCAAGAAGCTGCGCTCCTCTACATCTCCATCTGCAACCGCGAGATCTCGCCCA 2160
 173 N C K K L R S S Y I S I C N R E I S P T 192

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FIG.14G

2161 CCGAGCGCTGCAACCGCGCAAGTGCCACAAGGCCCTGGCCAGTTCTTCGACCGGTGC 2220
193 E R C N R R K C H K A L R Q F F D R V P 212

2221 CCAGCGAGTACACCTACCGCATGCTCTTCTGTCTCCTGCCAAGACCAGGCGTGGCTGAGC 2280
213 S E Y T Y R M L F C S C Q D Q A C A E R 232

2281 GCCGCCGGCAAACCATCCTGCCCCAGCTGCTCCTATGAGGACAAGGAGAAGCCCAACTGCC 80 / 135
233 R R Q T I L P S C S Y E D K E K P N C L 2340
252 252

2341 TGGACCTGCGTGCGGTGTCGGGACTGACCCACCTGTGTGTCGGTCCCGGCTGGCCGACTTCC 2400
253 D L R G V C R T D H L C R S R L A D F H 272

2401 ATGCCAATTGTCGAGCCTCCTACCAGACGGTCAACCAGCTGCCCTGCGGACAATTACCAGG 2460
273 A N C R A S Y Q T V T S C P A D N Y Q A 292

FIG. 14H

2461 CGTGTCTGGGCTCTTATGCTGGCATGATTGGGTTTGACATGACACCTAACTATGTGGACT 2520
293 C L G S Y A G M I G F D M T P N Y V D S 312

2521 CCAGCCCCACTGGCATCGTGGTGTCCCCCTGGTGCAGCTGTCTGTCGGCAGCGGGAACATGG 2580
313 S P T G I V V S P W C S C R G S G N M E 332

2581 AGGAGGAGTGTGAGAAAGTTCCCTCAGGGACTTCACCGAGAACCCCATGCCCTCCGGAACGCCA 2640
333 E E C E K F L R D F T E N P C L R N A I 352

2641 TCCAGGCCTTTGGCAACGGCACGAACGTGAACGTGTCCCCCAAAGGCCCTCGTTCCAGG 2700
353 Q A F G N G T N V N V S P K G P S F Q A 372

2701 CCACCCAGGCCCTCGGGTGGAGAAGACGCCTTCTTTGCCAGATGACCTCAGTGACAGTA 2760
373 T Q A P R V E K T P S L P D D L S D S T 392

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FIG. 14I

2761 CCAGCTTGGGACCAGTGTCTCATCACCACTGCACGTCTGTCCAGGAGCAGGGGCTGAAGG 2820
393 S L G T S V I T T C T S V Q E Q G L K A 412

2821 CCAACAACCTCCAAAGAGTTAAGCATGTGCTTCACAGAGCTCACGACAAATATCATCCCAG 2880
413 N N S K E L S M C F T E L T T N I I P G 432

2881 GGAGTAACAAGGTGATCAAAACCTAACTCAGGCCCCAGCAGACCGTCGGCTGCCT 2940
433 S N K V I K P N S G P S R A R P S A A L 452

2941 TGACCGTGCTGTCTCCTGATGCTGAAACTGGCCTTGTAGGCTGTGGGAACCGAGTCAG 3000
453 T V L S V L M L K L A L * 464

3001 AAGATTTTGAAGCTACGCAGACAAGAACAGCCGCCCTGACGAAATGGAACACACACAG 3060

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FIG. 14J

3061 ACACACACACCTTGCAAAAAAATTGTTTTTCCACCTTGTCGCTGAACCTGTCTC 3120
3121 CTCCCAGGTTTCTCTCTGGAGAAGTTTTTGTAACCAACAGACAAGCAGGCAGCAGC 3180
3181 CTGAGAGCTGGCCAGGGGTCCCCTGGCAGGGGAACTCTGGTGCCGGGAGGCACGAG 3240
3241 GCTCTAGAAAATGCCCTTCACTTTCTCCTGGTGTTTTTCTCTCTCTGACCCCTTCTGAAGCAG 3300
3301 AGACCGGACAAGAGCCTGCAGCGGAAGGACTCTGGGCTGTGCCCTGAGGCTGGCTGGGGG 3360
3361 CAGGACAACACAGCTGCTTCCCCAGGCTGCCCACTCTGGGGACCCGCTGGGGCTGGCAG 3420
3421 AGGGCATCGGTCAGCGGGGCAGCGGGGCTGGCCATGAGGGTCCACCTTCAGCCCTTTGGC 3480

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FIG. 14K

3481 TTCAAGGATGGAGATGGTTTGTGCCCCCTCCCTCTCTGCCCCCTCGGGTGGGGCTGGTGGGCTCTG 3540
3541 CAGCTGGTGTGGGAACCTTCCCCACGGAATGGCGGTGGAGGGGTTCCGACCGTGTGGTGGGCT 3600
3601 CCCCCTGA CTGACGAGAGTGTGGGGCTGGGGCCAGCTCCAGGAGGGCTTGAGAGC 3660
3661 TCAGCCTGCCCTGGGAGAGCCCTTGTGGCGAGGCATTAAAACTTGGGCACCACTTCTTTC 3720
3721 TCGGTGGCAGAAATTTGAAGTCAGAGAGAAACGGTCCTTTGTGGCTTCTTTGCTTCT 3780
3781 CGTGGGTCCCTTTGGCAGGCCCTCCCTTTGGGAGAGGGAGAGACCAAGCCGGGTG 3840
3841 TGTGTCTGCAGCACCGTGGGCCCTCAAGCTTTCCCTGCTCTTCTCCCTCCTCCTCTT 3900

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FIG. 14L

3901 CCCCTTCTCTTTCCTCATTTCCCTAGACGTACGTCAACTGTATGTACATACCGGGGCTCC 3960
3961 TCTCCTAACATATATGTATATACACATCCATATACATATATTTGGTGTGTTTCCCTTTCT 4020
4021 TTCCCTTTTAAAGCAACAACCTATGGAATAATACCCCAACAGATGAGCGAAATGTA 4080⁸⁵ / 135
4081 TTATTGTAAAGTTTATTTTAACTGTTGTCTATAATGGGGAAAAAGGACATTGGC 4140
4141 CCCGCAGTGCCCTGCCCCAGTCAGCCTGGCTGGCTCTGTGTGGGGCTCCTGATCCGCAT 4200
4201 CCAAGCTTAACCAAGGCTCCAATAAACGTGCG 4232

FIG. 15A

Human GRR3

1 CAAGTCAAAGGTTTAATCATGATCCAAGAGCCCAAGAGAGACTTTAGGACAAATAAGGAA 60

61 TAAAGCAAGGCCACAGGCTCCAGCTCCTGATGCCCAAGATGTTCCGGCAGGATCCGGGGAC 120

121 AGGCGAGTGCAGGCAGTAGTTTTCATCCTCCATCCAGGGAGGAGCGAGCGCGG 180

181 AGCCCGGCGCCTACAGCTCGCCATGGTGGCCCCCTGAACCCGCGACCGCTGCCGCCCGT 240
1 M V R P L N P R P L P P V 13

241 AGTCCTGATGTTGCTGCTGCTGCCCGCTCGCCGCTGCCCTCTCGCAGCCGGAGACCC 300
14 V L M L L L L P P S P L P L A A G D P 33

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FIG. 15B

301 CCTTCCACAGAAAGCCGACTCATGAACAGCTGTCTCCAGGCCAGGAGGAAGTGCCAGGC 360
34 L P T E S R L M N S C L Q A R R K C Q A 53

361 TGATCCCACTGCAGTGCTGCCTACCAACCACTGGATTCCCTGCACCTCTAGCATAAGCAC 420
54 D P T C S A A Y H H L D S C T S S I S T 73

421 CCCACTGCCCTCAGAGGAGCCCTTCGGTCCCCTGCTGACTGCCCTGGAGGCAGCACAGCAACT 480
74 P L P S E E P S V P A D C L E A A Q Q L 93

481 CAGGAACAGCTCTCTGATAGGCTGCATGTGCCACCCGCCGCATGAAGAACCAGGTTGCCCTG 540
94 R N S S L I G C M C H R R M K N Q V A C 113

541 CTTGGACATCTATTGGACCGTTCAACCGTGCCCGCAGCCCTTGGTAACATAGAGCTGGATGT 600
114 L D I Y W T V H R A R S L G N Y E L D V 133

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FIG.15C

601 CTCCCCCTATGAAGACACAGTGACCAAGCAACCTGGAAATGAATCTCAGCAAACTGAA 660
134 S P Y E D T V T S K K P W K M N L S K L N 153

661 CATGCTCAAACCACTCAGACCTCTGCCCTCAAGTTTGCCATGCTGTGTACTCTCAATGA 720
154 M L K P D S D L C L K F A M L C T L N D 173

721 CAAGTGTGACCGGCTGCGCAAGGCCCTACGGGAGGCGTGCTCCGGGCCCCACTGCCAGCG 780
174 K C D R L R K A Y G E A C S G P H C Q R 193

781 CCACGTCTGCCCTCAGGCAGCTGCTCACTTTCTTCGAGAAGGCCCGCCGAGCCCCACGCGCA 840
194 H V C L R Q L L T F F E K A A E P H A Q 213

841 GGGCCTGCTACTGTGCCCATGTGCCCCCCAACGACCGGGGCTCGGGGAGCGCGCGCAA 900
214 G L L C P C A P N D R G C G E R R N 233

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FIG.15D

901	CACCATGCGCCCAACTGCGCGCTGCGCGCTGTGGCCCCCAACTGCCTGGAGCTGCGGCG	960
234	T I A P N C A L P P V A P N C L E L R R	253
961	CCTCTGCTTCTCCGACCCCGCTTTGCAGATCACGCCCTGGTGGATTTCACAGACCCACTGCCA	1020
254	L C F S D P L C R S R L V D F Q T H C H	273
1021	TCCCATGGACATCCCTAGGAACCTTGTGCAACAGAGCAGTCCAGATGTCTACGAGCATACCT	1080
274	P M D I L G T C A T E Q S R C L R A Y L	293
1081	GGGGCTGATTGGGACTGCCATGACCCCAACTTTGCCAGCAATGTCAACACCAGTGTTC	1140
294	G L I G T A M T P N F A S N V N T S V A	313
1141	CTTAAGCTGCACCTGCCAGGCAGTGGCAACCTGCAGGAGGAGTGTGAAATGCTGGAAGG	1200
314	L S C T C R G S G N L Q E E C E M L E G	333

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FIG.15E

1201 GTTCTTCTCCACAACCCCTGCCCTCACGGAGGCCATTGCAGCTAAGATGCCGTTTTCACAG 1260
334 F F S H N P C L T E A I A A K M R F H S 353

1261 CCAACTCTTCTCCAGGACTGGCCACACCCCTACCTTTGCTGTGATGGCACACCAGAATGA 1320
354 Q L F S Q D W P H P T F A V M A H Q N E 373

1321 AAACCCTGCTGTGAGGCCACAGCCCTGGGTGCCCTCTCTTTCTCCTGCACGCTTCCCTT 1380
374 N P A V R P Q P W V P S L F S C T L P L 393

1381 GATTCTGCTCCTGAGCCTATGGTAGCTGGACTTCCCCAGGCCCTCTTCCCCCTCCACCAC 1440
394 I L L S L W * 400

1441 ACCCAGGTGGACTTGCAGCCACAGGGGTAGGAAAGGACAGCAGCAGGAAGGAGGTGC 1500

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FIG. 15F

1501 AGTGCGCAGATGAGGGCACAGGAGAAGCTAAGGGTTATGACCTCCAGATCCTTACTGGTC 1560
1561 CAGTCCCTCATTTCCCTCCACCCCATCTCCACTTCTGATTCA TGCTGCCCTCCTTGTTGGC 1620
1621 CACAATTTAGCCATGTCACTCTGGTGGTGACCAAGCTCCACCAAGCCCCCTTTGTGAGCCCTT 1680
1681 CCTCTTGACTACCAGGATCACCCAGAACTCTAATAAGTTAGCCCTTCTCTATTGCAATCCAG 1740
1741 ATTAGGGTTAGGGTAGGGAGGACTGGGTGTTCTGAGGCAGCCTAGAAAGTCATTCCTCCTT 1800
1801 TGTGAAGAAGGCTCCTGCCCCCCTCGTCTCCTCCTGAGTGGAGGATGGAATAACTACTGC 1860
1861 CTGCACTGCCCTGTCCCCGGATCCTGCCGAACATCTGGGCATCAGGAGCTGGAGCCCTGTG 1920

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FIG.15G

1921 GGCCCTTGCTTTATTCCCTATTATTGTCCTAAAGTCTCTCTGGGCTCTTGGATCATGATTAA 1980

1981 ACCTTTGACTG 1991

FIG. 16A

Rat GRR2

1 GCGGCCGCGTCGACCTTGACCATGCAGACACTTTTTCAGGCCCTCTGTCTGGTGTGAAGTT 60

61 GGCAGATACAAGCAAGGCCCGAAGGGTCTCAGCTTCTCTCCTGGCCTCCTGGACT 120

121 GAGTTAGGCTTGCTTCTGGTTGTCTTCTAAAGGCACGGTGATACAGAATGATGAGACTAG 180

181 GCTGGAGGGGCTTTCTGCTTCTGTGTGACCTTGAGTTATCTCCCTTCGTTGGATC 240

241 CGAGCTTTCCTGGAATATGATGTTGAATATGAATATGAGTTCTGCCTAAGGTCCAGACAG 300

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FIG. 16B

301 GCTCTGAGGGTTAACTGACTTTTGGAGCCTTTCAAATCAATACCTTGGATGGAGTGGGGGT 360
361 TTGTCCAATGGGAGTTGAGGCAAGATCCCTTTGCATAAGCCTTGCCACATCATGTTGAAG 420
421 CCATGCCATTCTGTCTGGACTATTGGCATCTTACCCTTTCAGCAGTTTCAGTGAAGCCCT 480
481 TCCTGGATTATCATCTCTGTGTTCCACTGCCCTAGGATTGTGCTCAAGAGGAATGAATGT 540
541 GAACCATGGTTGTAGGGAGTATGGCCAAACCAGGTTGGGTCTGTGTTGACCTTGGTCTTG 600
1 M V V G E Y G Q P G W V C V D L G L G 19
601 GTGTTCTTTTGTAAAGTGGGTGAGAAAGTTCCCTTCAAACCTTAGGCCCTACATTGGGGTC 660
20 V L L C K V G E K F L Q T L G L H W G Q 39

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FIG. 16C

661 AGAGACTGTGGTGGCCCTCATTCATGCTTGCTCTCCCTTCCCACTACCCAGACGAAACCC 720
40 R L W P S F M L V F P S H Y P D E T L 59

721 TCCGCTCTTTGGCCAGCCCTTCCCTCCCTGCAGGGCTCTGAGCTCCACGGCTGGCGCCCCC 780
60 R S L A S P S S L Q G S E L H G W R P Q 79

781 AAGTGGACTGTGTCCGGGCCAATGAGCTGTGTGCGGCTGAATCCAACCTGCAGCTCCAGGT 840
80 V D C V R A N E L C A A E S N C S S R Y 99

841 ACCGCACCCTTCGGCAGTGCCCTGGCAGGCCGGGATCGCAATACCATGCTGGCCAATAAGG 900
100 R T L R Q C L A G R D R N T M L A N K E 119

901 AGTGCCAGGCAGCCCTGGAGGTCTTGCAGGAAGCCCACTGTATGACTGCCGCTGCAAGC 960
120 C Q A A L E V L Q E S P L Y D C R C K R 139

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FIG.16D

961 GGGCATGAAGAGGCTGCAGTGTCTGCAGATCTACTGGAGCATCCATCTGGGGCTGA 1020
140 G M K K E L Q C L Q I Y W S I H L G L T 159

1021 CAGAGGTGAGGAGTTCTATGAAGCTTCCCCCTATGAGCCTGTGACCTCGCGCCTCTCGG 1080
160 E G E E F Y E A S P Y E P V T S R L S D 179

1081 ACATCTTCAGGCTCGCTTCAATCTTCTCAGGGACAGGGACAGACCCGGGTCAGTACCA 1140
180 I F R L A S I F S G T G T D P A V S T K 199

1141 AAAGCAACCACTGCCCTGGATGCCCGCCAAAGCCCTGCAACCTGAATGACAACTGCAAGAAGC 1200
200 S N H C L D A A K A C N L N D N C K K L 219

1201 TTCGCTCCCTCTTATATCTCCATCTGCAACCGTGAGATCTCTCCACCGAACGCTGCAACC 1260
220 R S S Y I S I C N R E I S P T E R C N R 239

FIG. 16E

1261	GCCGCAAGTGCCACAAGGCTCTGCGCCAGTTCTTTGACCGTGTGCCAGCGAGTATACCT	1320
240	R K C H K A L R Q F F D R V P S E Y T Y	259
1321	ACCGCATGCTCTTCTGCTCCTGTGTCAGGACGAGGCATGTGCTGAGCGTCCGCGCAACCA	1380
260	R M L F C S C Q D Q A C A E R R R Q T I	279
1381	TCCTGCCCCAGTTGCTCCTATGAGACAAGGAGAAGCCCAACTGCCCTGGACCTGCCGAGCC	1440
280	L P S C S Y E D K E K P N C L D L R S L	299
1441	TGTGTCGTACAGACCACCTGTGCGCGGTCCCGACTGGCAGATTTCCACGCCCACTGTCGAG	1500
300	C R T D H L C R S R L A D F H A N C R A	319
1501	CCTCCTACCGGACAATCACCAGCTGTCTGCGGACAACCTACCAGGCATGTCTGGGCTCCT	1560
320	S Y R T I T S C P A D N Y Q A C L G S Y	339

9 7 5

FIG.16F

1561 ATGCTGGCATGATTGGGTTTGATATGACACCCAACCTATGTGGACTCCAAACCCACGGGCA 1620
340 A G M I G F D M T P N Y V D S N P T G I 359

1621 TCGTGGTGTCCTCCCTGGTGCAATTGTCGTGGCAGTGGGAACATGGAAGAAGAGTGTGACA 1680
360 V V S P W C N C R G S G N M E E C E K 379

1681 AGTTCCTCAGGACTTCACGGAAACCCCATGCGCTCCGGAATGCCATTTCAGGCCTTTGGTA 1740
380 F L R D F T E N P C L R N A I Q A F G N 399

1741 ATGGCACAGATGTGAACATGTCTCCCAAAGGCCCTCAGCTCCAGCTACCCAGGCCCTC 1800
400 G T D V N M S P K G P S L P A T Q A P R 419

1801 GGGTGGAGAAGACTCCTTCACTGCCAGATGACCTCAGTGACAGCACAGCCTGGGGACCA 1860
420 V E K T P S L P D D L S D S T S L G T S 439

1861 GTGTCATCACCTGCACATCTATCCAGGAGCAAGGGCTGAAGGCCCAACAACTCCAAAG 1920

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FIG. 16G

440 V I T T C T S I Q E Q G L K A N N S K E 459

1921 AGTTAAGCATGTGCTTCACAGAGCTCACGACAAACATCAGTCCAGGAGTAAAAAGGTGA 1980
460 L S M C F T E L T T N I S P G S K K V I 479

1981 TCAAACTTAACTCAGGCTCCAGCAGAGCCAGACTGTGCGCTGCCCTTGACTGCCCTCCAC 2040
480 K L N S G S S R A R L S A A L T A L P L 499

2041 TCCTGATGCTGACCTTGGCCTTGTAGGCCTTTGGAACCCAGCACAAAAGTTCTTCAAGCA 2100
500 L M L T L A L * 506

2101 ACCCAGATATGAAC TCCCGCTGACAAAATGGAAACACACGCATACACATGCCACACA 2160

2161 CAGACACACACAGACACACACACACACATACAGACGTCGACCGGCCGC 2215

FIG.17A

Rat GFR3

1 GCGGCCGCGTCGACCGACGCCAGCCAGCACAGGCAGAGCGCTGCCGGGTCCGCGGCTCCAGA 60

61 CCCGCCATGGGGCTCTCCCGGAGCCCGCGACCGCCGCGCTAGTGATCCTGCTACTGGTG 120
1 M G L S R S P R P P P L V I L L L V 18

121 CTGTCGCTGTGGCTACCCCTTGGAACAGGAACTCCCTTCCACAGAGAACAGGCTTGTG 180
19 L S L W L P L G T G N S L P T E N R L V 38

181 AACAGCTGTACCCAGGCCAGAAAAATGCGAGGCTAATCCCGCTTGCAAGGCTGCCTAC 240
39 N S C T Q A R K K C E A N P A C K A A Y 58

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FIG.17B

241 CAGCACCTGGACTCCTGCACCCCCAGTCTCAGCAGTCCACTGCCCTCAGGGAGTCTGCC 300
59 Q H L D S C T P S L S S P L P S G E S A 78

301 ACATCTGCAGCGTGCCTTGAAGCAGCACAGCAACTCAGGAACAGCTCTCTCATAGACTGC 360
79 T S A A C L E A A Q Q L R N S S L I D C 98

361 AGGTGCCACCGCGCATGAAGCACCACCAAGCTACCTGTCTGTGACATTATTGGACCGTTCAC 420
99 R C H R R M K H Q A T C L D I Y W T V H 118

421 CCTGTCCGAAGCCTTGGTGACTACGAGTTGGACGTCTCACCCCTATGAAGACACAGTGACC 480
119 P V R S L G D Y E L D V S P Y E D T V T 138

481 AGCAAACCCCTGGAAAATGAATCTCAGCAAGCTGAGCATGCTCAAACCAAGACTCCGACCTC 540
139 S K P W K M N L S K L S M L K P D S D L 158

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FIG.17C

541	TGCCTCAAATTGCTATGCTGTGTACTCTTAACGACAAGTGGACCGCCTCCGAAAGGCC	600
159	C L K F A M L C T L N D K C D R L R K A	178
601	TACGGGAGGCGTGCTCAGGGATCCGCTGCCAGCGCCACCTCTGCTAGCTCAGCTGCGC	660
179	Y G E A C S G I R C Q R H L C L A Q L R	198
661	TCCTTCTTCGAGAAGGCGGCAGAGTCCACGCTCAGGGCCTGCTGTGTCCCTGTGCA	720
199	S F F E K A A E S H A Q G L L L C P C A	218
721	CCCGAAGATGCGGCGCTGTGGGAGCGCGCGCAACACCATCGCCCCCAGTTGCGCCCTC	780
219	P E D A G C G E R R R N T I A P S C A L	238
781	CCGTCTGTGGCCCCAACTGCCTAGATCTTCGGAGCTTCTGCCGTGCGGACCCCTCTGTGC	840
239	P S V A P N C L D L R S F C R A D P L C	258

1 0 2 / 1 3 5

FIG. 17E

1141 GACTCTACTTTTCTGTGATGCAGCAGCAGACAGACGCCCTGCTCTGAGGCCCCAGCTC 1200
359 D S T F S V M Q Q Q N S S P A L R P Q L 378

1201 AGGCTACCCGTTCTGTCTTTCTTTCATCCTTACCTTGATTCTGCTGCAGACCCCTCTGGTAA 1260
379 R L P V L S F F I L T L I L L Q T L W * 397

1261 CTGGGCTCCCCTCAGGGTCCTTTGTCTCTCTCCACACACCCAGACCGACTTGCAGCCCTGTG 1320 0 4 / 1 3 5
1321 ATGGGAGAGAAAATGCTGGCCCTCTGGAAGAAGATGCAACCAGGCTCACTGCACATCCTGT 1380

1381 CTGCTCCAGATGAGGTCTTGGAAAGACGAGGGCTGTGACCGTTCAGAAATCCTGAGCGGC 1440

1441 CAGCTTCAACCTCTCCTACTTACTCCTGCTTGGGCTGCTCCTCCCTAGGACCTTGTTAC 1500

FIG.17D

841	AGATCAGCCCTGATGGACTTCCAGACCCCACTGCCACCCCTATGACATCCTCGGACTTGT	900
259	R S R L M D F Q T H C H P M D I L G T C	278
901	GCAACTGAGCAGTCCAGATGTCTGCGGGCATACTGCGGGCTAATTGGGACTGCCATGACC	960
279	A T E Q S R C L R A Y L G L I G T A M T	298
961	CCAAACTTCATCAGCAAGGTCAACACTACTGTGCGCTTAGGCTGTACCTGCCGAGGCAGT	1020
299	P N F I S K V N T T V A L G C T C R G S	318
1021	GGCAACCTGCAGGACGAGTGTGAACAGCTGGAAAAGTCCTTCTCCAGAACCCCTGCCTC	1080
319	G N L Q D E C E Q L E K S F S Q N P C L	338
1081	ATGAGGCCATTGCGGCTAAATGCGGTTTCCACAGACAACCTCTTCTCCAGGACTGGGCG	1140
339	M E A I A A K M R F H R Q L F S Q D W A	358

1 0 3 / 1 3 5

FIG.17F

1501 TCCAGTTGGCTGTATATTGTGGTGGTGATTAGCTTCCCACCTCCAGCCCCTTCTTCCTGT 1560

1561 TTCCCAGGACCAACCAGGGCTAATGACTCACTCAATTCCTGGTTGCCCTTCTCCAGGAAGGC 1620

1621 AGGCTGAGGGTTCTGAGGCAGCTGAGAAAGATGGTCCCTTTGTGAGGAAGGCTGGTGGTC 1680

1681 CAACCGTCGACGGGCCG 1699

1 0 5 / 1 3 5

1 0 6 / 1 3 5

FIG.18A

Alignment of the Amino Acid Sequences of GDNFRs

1				50
Mgdnfr	~~~~~	~~~~~MFLATL	YFVLPLLDLL	MSAEVSG.GD RLDCVKASDQ
Rgdnfr	~~~~~	~~~~~MFLATL	YFALPLLDLL	MSAEVSG.GD RLDCVKASDQ
Hgdnfr	~~~~~	~~~~~MFLATL	YFALPLLDLL	LSAEVSG.GD RLDCVKASDQ
Hgrr2	~~~~~MILANV	FCLFFFLDDT	LRSLASPSSL	QGPELHGWRP PVDCVRANEL
Rgrr2	~~~~~ML	VFPSHYPDET	LRSLASPSSL	QGSELHGWRP QVDCVRANEL
Hgrr3	MVRPLNPRPL	PPVVLMLLLL	LPSPPLPLAA	GDPPLPTESRL MNSCLQARRK
Rgrr3	MGLSRSPRPP	PLVILLLVLS	L...WLPLGT	GNSLPTENRL VNSCTQARRK

FIG. 18B

51 100

Mgdnfr CLKEQSCSTK YRTLQCVAG KETNFSLTSG LEAKDECRSA MEALKQKSLY

Rgdnfr CLKEQSCSTK YRTLQCVAG KETNFSLTSG LEAKDECRSA MEALKQKSLY

Hgdnfr CLKEQSCSTK YRTLQCVAG KETNFSLTSG LEAKDECRSA MEALKQKSLY

Hgrr2 CAAESNCSSR YRTLQCLAG RDRNTML... ..ANKECQAA LEVLQESPLY

Rgrr2 CAAESNCSSR YRTLQCLAG RDRNTML... ..ANKECQAA LEVLQESPLY

Hgrr3 CQADPTCSAA YHLDSCSTSS ISTPLP.SEE PSVPADCLEA AQQLRNSSLI

Rgrr3 CEANPACKAA YHLDSCSTPS LSSPLP.SGE SATSAACLEA AQQLRNSSLI

1 0 7 / 1 3 5

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FIG.18C

	101		150
Mgdnfr	NCRCKRGMKK	EKNCLRIYWS	MYQSL.QGND LLEDSPYEPV NSRLSDIFRA
Rgdnfr	NCRCKRGMKK	EKNCLRIYWS	MYQSL.QGND LLEDSPYEPV NSRLSDIFRA
Hgdnfr	NCRCKRGMKK	EKNCLRIYWS	MYQSL.QGND LLEDSPYEPV NSRLSDIFRV
Hgrr2	DCRCKRGMKK	ELQCLQIYWS	IHLGLTEGEE FYEASPYEPV TSRLSDIFRL
Rgrr2	DCRCKRGMKK	ELQCLQIYWS	IHLGLTEGEE FYEASPYEPV TSRLSDIFRL
Hgrr3	GCMCHRRMKN	QVACLDIYWT	VHRARSLGNY ELDVSPYE...DTVTS
Rgrr3	DCRCHRRMKH	QATCLDIYWT	VHPVRSGLDY ELDVSPYE...DTVTS

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FIG.18D

	151	200
Mgdnfr	VPFISDVFQQ VEHISKGNNC LDAAKACNLD DTCKKYRSAY ITPCTTSM.	
Rgdnfr	VPFISDVFQQ VEHISKGNNC LDAAKACNLD DTCKKYRSAY ITPCTTSM.	
Hgdnfr	VPFISDVFQQ VEHIPKGNNC LDAAKACNLD DICKKYRSAY ITPCTTSVS.	
Hgrr2	ASIFSGTGAD PVVSAKSNHC LDAAKACNLD DNCKKLRSY ISICNREISP	
Rgrr2	ASIFSGTGTD PAVSTKSNHC LDAAKACNLD DNCKKLRSY ISICNREISP	
Hgrr3	KPWKMNL SKL NMLKPDSDL C LKFAMLCTLN DKCDRLRKAY GEACS.....	

1 1 0 / 1 3 5

FIG. 18E

Rgrr3 KPWKMNLSKL SMLKPDSDLC LKFAMLCTLN DKCDRLRKAY GEACS.....

201 250

Mgdnfr NEVCNRRKCH KALRQFFDKV PAKHSYGM LF CSC..RDVAC TERRRQTIVP

Rgdnfr NEVCNRRKCH KALRQFFDKV PAKHSYGM LF CSC..RDIAC TERRRQTIVP

Hgdnfr NDVCNRRKCH KALRQFFDKV PAKHSYGLF CSC..RDIAC TERRRQTIVP

Hgr2 TERCNRRKCH KALRQFFDRV PSEYTYRMLF CSC..QDQAC AERRRQTILP

Rqrr2 TERCNRRKCH KALRQFFDRV PSEYTYRMLF CSC..QDQAC AERRRQTILP

Hqrr3 GPHCQRHVCL RQLLTFFEKA AEPHAQGLL CPÇAPNDRGC GERRRNTIAP

Rgr3 GIRCQRHLCL AQLRSFFEKA AESHAQGLLL CPCAPEDAGC GERRNTIAP

FIG.18F

	251		300
Mgdnfr	VCSYEERERP NCLNLQDSCK TNYICRSRLA DFFTNCQPE	RSVSNCLKEN	
Rgdnfr	VCSYEERERP NCLSLQDSCK TNYICRSRLA DFFTNCQPE	RSVSNCLKEN	
Hgdnfr	VCSYEEREKP NCLNLQDSCK TNYICRSRLA DFFTNCQPE	RSVSSCLKEN	
Hgrr2	SCSYEDKEKP NCLDLRGVCR TDHLCSRLA DFHANCRA	SY QTVTSCPADN	
Rgrr2	SCSYEDKEKP NCLDLRSLCR TDHLCSRLA DFHANCRA	SY RTITSCPADN	
Hgrr3	NCALPP.VAP NCLELRRLCF SDPLCSRLV DFQTHCHP..	MDILGTCATE	
Rgrr3	SCALPS.VAP NCLDLRSFCR ADPLCSRLM DFQTHCHP..	MDILGTCATE	

1 1 1 / 1 3 5

1 1 2 / 1 3 5

FIG.18G

	301		350
Mgdnfr	YADCLLAYSG	LIGTVMTTPNY	VDSS..SLSV APWCDCSNSG NDLEDCLKFL
Rgdnfr	YADCLLAYSG	LIGTVMTTPNY	VDSS..SLSV APWCDCSNSG NDLEDCLKFL
Hgdnfr	YADCLLAYSG	LIGTVMTTPNY	IDSS..SLSV APWCDCSNSG NDLEECCLKFL
Hgrr2	YQACLSYAG	MIGFDMTPNY	VDSSPTGIVV SPWCSCRGSG NMEECEKFL
Rgrr2	YQACLSYAG	MIGFDMTPNY	VDSNPTGIVV SPWCNCRGSG NMEECEKFL
Hgrr3	QSRCLRAYLG	LIGTAMTPNF	ASNVTSTVAL S..CTCRGSG NLQEECEMLE
Rgrr3	QSRCLRAYLG	LIGTAMTPNF	ISKVNTTVAL G..CTCRGSG NLQDECEQLE

FIG. 18H

351 400
Mgdnfr NFFKDNTCLK NAIQAFNGS DVTMWQPAP. PVQTTTATTT TAARIKKNKPS
Rgdnfr NFFKDNTCLK NAIQAFNGS DVTMWQPAP. PVQTTTATTT TAARVKNKPL
Hgdnfr NFFKDNTCLK NAIQAFNGS DVTVWQPAF. PVQTTTATTT TALRVKNKPL
Hgrr2 RDFTENPCLR NAIQAFNGT NVNVSPKGP. SFQATQAPRV EKTPSLPDDL
Rgrr2 RDFTENPCLR NAIQAFNGT DVNMSPKGP. SLPATQAPRV EKTPSLPDDL
Hgrr3 GFFSHNPCLT EAIAAKMRFH SQLFSQDWPH PTFAVMAHQN ENPAVRPQPW
Rgrr3 KSFSQNPCLM EAIAAKMRFH RQLFSQDWAD STFSVMQQQN SSPALRPQLR

1 1 3 / 1 3 5

FIG. 18I

401 450

Mgdnfr GPACSENEIP THVLPPCANL QAQKLKSNVS GSTHLCCLSDN DYGKDGCLAGA 1 1 4 / 1 3 5

Rgdnfr GPAGSENEIP THVLPPCANL QAQKLKSNVS GSTHLCCLSDS DFGKDGCLAGA

Hgdnfr GPAGSENEIP THVLPPCANL QAQKLKSNVS GNTHLCISNG NYEKEGL.GA

Hgrr2 SDSTS...LG TSVITTTCTSV QEQGLKANNS KELSMCFTEL TTNIIPGSNK

Rgrr2 SDSTS...LG TSVITTTCTSI QEQGLKANNS KELSMCFTEL TTNISPGSKK

Hgrr3 VPSLFSC TLP LILLSLW~~ ~~~~~~

Rgrr3 LPVLSFFILT LILLQTLW*~ ~~~~~~

1 1 5 / 1 3 5

FIG. 18J

	451		490
Mgdnfr	SSHITTKSMA APPSCGLSSL PVMVFTALAA	LLSVSLAETS	
Rgdnfr	SSHITTKSMA APPSCSLSSL PVLMLTALAA	LLSVSLAETS	
Hgdnfr	SSHITTKSMA APPSCGLSPL LVLVVTALST	LLSLTETS~~	
Hgrr2	VIKPNNGPSR ARPSAALTVL SVLMLKLAL*	~~~~~	
Rgrr2	VIKLNNGSSR ARLSAALTAL PLLMLTLAL*	~~~~~	
Hgrr3	~~~~~	~~~~~	
Rgrr3	~~~~~	~~~~~	

FIG. 19A

GDNFR Family of Receptors

1 50

Consensus MV..l...p .pp...m.l. llsalPl.. .lqgael.g. .Rl...dCv.A.
1 1 6 / 1 3 5

Hgdnfr MFLAT LYFALPLLLDL LLSAEVSGGD RL..DCVKAS
Rgdnfr MFLAT LYFALPLLLDL LMSAEVSGGD RL..DCVKAS

Hgrr2 MILANVF CLFFFLDDTL RSLASPSS.. LQPELHW. RPPVDCVRAN
Rgrr2 MLV FPSHYPDETL RSLASPSS.. LQSELHW. RPQVDCVRAN

Hgrr3 MVRPLNPRPL PPVVLMLLLL LPPS.PLP.L AAGDPLPTES RLMNSCLQAR
Rgrr3 MGLSRSPR PPPLVILLLV LSLWLPLG.. .TGNSLPTEN RLVNSCTQAR

FIG. 19B

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	51		100
Consensus	..C.ae..Cs ..YrtLrqC. ag...nt.La sg.E..... C..A.e.L..		
Hgdnfr	DQCLKEQSCS TKYRTLQCV AGKETNFSLA SGLEAKDE.. CRSAMEALKQ		
Rgdnfr	DQCLKEQSCS TKYRTLQCV AGKETNFSLT SGLEAKDE.. CRSAMEALKQ		
Hgrr2	ELCAAESNCS SRYRTLQCL AGRDRNTMLA NK.E..... CQAALEVLQE		
Rgrr2	ELCAAESNCS SRYRTLQCL AGRDRNTMLA NK.E..... CQAALEVLQE		
Hgrr3	RKCQADPTCS AAYHHLDST ..SSISTPLP SE.EPSVPAD CLEAAQQLRN		
Rgrr3	KKCEANPACK AAYQHLDST ..PSLSSPLP SG.ESATSAA CLEAAQQLRN		

FIG.19C

	101		150
Consensus	ssLydCrCkR	gmkke..CL. IYws.h..l. .Gn..le.SP	YEP.VtSrls
Hgdnfr	KSLYNCRCKR	GMKKEKNCLR IYWSMYQSLQ .GNDLLEDSP	YEP.VNSRLS
Rgdnfr	KSLYNCRCKR	GMKKEKNCLR IYWSMYQSLQ .GNDLLEDSP	YEP.VNSRLS
Hgrr2	SPLYDCRCRK	GMKKELQCLQ IYWSIHLGLT EGEEFYEASP	YEP.VTSRLS
Rgrr2	SPLYDCRCRK	GMKKELQCLQ IYWSIHLGLT EGEEFYEASP	YEP.VTSRLS
Hgrr3	SSLIGCMCHR	RMKNQVACL D IYWTVHRARS LGNYELDVSP	YEDTVTSKPW
Rgrr3	SSLIDCRCHR	RMKHQATCLD IYWTVHPVRS LGDYELDVSP	YEDTVTSKPW

1 1 8 / 1 3 5

FIG.19D

151

200

Consensus	difr...s...sd.....	kSn.CLdaAk	aCnLnD.Ckk	lRsaYi...C.	
Hgdnfr	DIFRVVPFIS	DVFQQVEHIP	KGNNCLDAAK	ACNLDDICKK	YRSAYITPCT	
Rgdnfr	DIFRAVPFIS	DVFQQVEHIS	KGNNCLDAAK	ACNLDDTCKK	YRSAYITPCT	1 1 9 / 1 3 5
Hgrr2	DIFRLASIFS	GTGADPVVSA	KSNHCLDAAK	ACNLNDNCKK	LRSSYISICN	
Rgrr2	DIFRLASIFS	GTGTDPAVST	KSNHCLDAAK	ACNLNDNCKK	LRSSYISICN	
Hgrr3	KMNL...SKLN	MLKPD.....	.SDLCLKFAM	LCTLNDKCDR	LRKAYGEAC.	
Rgrr3	KMNL...SKLS	MLKPD.....	.SDLCLKFAM	LCTLNDKCDR	LRKAYGEAC.	

FIG. 19E

	201		250	
Consensus	...S...erCn	RrkChkaLrq	FFdkvp...h.	ygmLfCsC... .D.aC.ERRRR
Hgdnfr	TSVS.NDVCN	RRKCHKALRQ	FFDKVPKHS	YGMLFCSC... RDIACERRR
Rgdnfr	TSMS.NEVCN	RRKCHKALRQ	FFDKVPKHS	YGMLFCSC... RDIACERRR
Hgrr2	REISPTECN	RRKCHKALRQ	FFDRVPSEYT	YRMLFCSC... QDQACAERRR
Rgrr2	REISPTECN	RRKCHKALRQ	FFDRVPSEYT	YRMLFCSC... QDQACAERRR
Hgrr3	...SG.PHCQ	RHVCLRQLLT	FFEKAAEPHA	QGLLLCPCAP NDRGCCERRR
Rgrr3	...SG.IRCQ	RHLCLAQLRS	FFEKAAESHA	QGLLLCPCAP EDAGCCERRR

1 2 0 / 1 3 5

FIG. 19F

	251	300
Consensus	qTI.PsCsye ..ekPNCLdL r..CrtD.lC RSRLaDF.tn C....r.v.s	
Hgdnfr	QTIVPVCSYE EREKPNCLNL QDSCKTNYIC RSRLADFFTN CQESRSVSS	1 2 1 / 1 3 5
Rgdnfr	QTIVPVCSYE ERERPNCLSL QDSCKTNYIC RSRLADFFTN CQESRSVSN	
Hgrr2	QTILPSCSYE DKEKPNCLDL RGVCRTDHLC RSRLADFHAN CRASYQTVTS	
Rgrr2	QTILPSCSYE DKEKPNCLDL RSLCRTDHL C RSRLADFHAN CRASYRTITS	
Hgrr3	NTIAPNC.AL PPVAPNCLEL RRLCFSDPLC RSRLVDFQTH C.HPMDILGT	
Rgrr3	NTIAPSC.AL PSVAPNCCLDL RSFCRADPLC RSRLMDFQTH C.HPMDILGT	

FIG.19G

301
Consensus C.a.ny..CL .ay.GlIGt. MTPNyvdss. t...VapwC. CrgSGN...ee 350
Hgdnfr CLKENYADCL LAYSLIGTV MTPNYIDSSS ..LSVAPWCD CSNSGNDLEE 1 2 2 / 1 3 5
Rgdnfr CLKENYADCL LAYSLIGTV MTPNYVDSSS ..LSVAPWCD CSNSGNDLED
Hgr2 CPADNYQACL GSYAGMIGFD MTPNYVDSSP TGIVVSPWCS CRGSGNMEEE
Rgr2 CPADNYQACL GSYAGMIGFD MTPNYVDSP TGIVVSPWCN CRGSGNMEEE
Hgr3 C.ATEQSRCL RAYLGLIGTA MTPNFASNPN TS..VALSCT CRGSGNLQEE
Rgr3 C.ATEQSRCL RAYLGLIGTA MTPNFISKVN TT..VALGCT CRGSGNLQDE

FIG. 19H

	351		400	
Consensus	Cekfl.ff..	NpCL.nAIqA	fgng.....	p.fsvt.t.a
Hgdnfr	CLKFLNFFKD	NTCLKNAlQA	FGNGS....D	VTWQPAFPV QTTATTTTA
Rgdnfr	CLKFLNFFKD	NTCLKNAlQA	FGNGS....D	VTWQPAPPV QTTATTTTA
Hgrr2	CEKFLRDFTE	NPCLRnAlQA	FGNGTNV...NVSP KGPSFQATQA
Rgrr2	CEKFLRDFTE	NPCLRnAlQA	FGNGTDV...NMSP KGPSLPATQA
Hgrr3	CEMLEGFFSH	NPCLTEAlAA	KMRFHSQLFS	QDWPHPTFAV MAHQENENPAV
Rgrr3	CEQLEKSFSQ	NPCLMEAlAA	KMRFHRQLFS	QDWADSTFSV MQQQNSSPAL

1 2 3 / 1 3 5

FIG.19I

401 450
Consensus .rv...PsL. ...s....l. t.v...C..l Q.Q.LK.N.S .e...Cf.el
Hgdnfr LRVKNKP.LG PAGSENEIP. THVLPPCANL QAQKLKSNVS GNTHLCISNG
Rgdnfr FRVKNKP.LG PAGSENEIP. THVLPPCANL QAQKLKSNVS GSTHLCCLSDS
Hgrr2 PRVEKTPSLP DDLSDESTSLG TSVITTTCTSV QEQLKANNS KELSMCFTEL
Rgrr2 PRVEKTPSLP DDLSDESTSLG TSVITTTCTSI QEQLKANNS KELSMCFTEL
Hgrr3 RPQPWVPSLF SCTLPLILL SLW
Rgrr3 RPQLRLPVLS FFILTILLQ TLW
451 499
Consensus ttn....sg. ...i....s.. A.pS.aL..L pvlmltala. LLS....S
Hgdnfr NYEKEGL.GA SSHITTKSMA APPSCGLSPL LVRVVTALST LLSLTETS
Rgdnfr DFGKDGLAGA SSHITTKSMA APPSCSLSSL PVLMLTALAA LLSVSLA
Hgrr2 TTNIIPGSNK VIKPNSGPSR ARPSAALTVL SVLMLK.LAL
Rgrr2 TTNISPGSKK VIKLNSGSSR ARLSAALTAL PLLMLTLAL

1 2 4 / 1 3 5

FIG. 20A

Human GDNFR α MELATLYFALPLLLDILLSAEVSGGDRLLDCVKASDQCLKE
 Rat GDNFR α MELATLYFALPLLLDILMSAEVSGGDRLLDCVKASDQCLKE
 Human GRR2 MILANVECLFFELDDTLRSLASPSLLQCFELHGWRRPVD CVRANELCAAE
 Rat GRR2 MLVFPSSHYPDETILRSLASPSLLQGSSELHGWRRPQVDCVRANELCAAE

Human GDNFR α QSCSTKYRTLRLQCVAGKETNFSIASGLEAKDECRSAMEALKQKSLYNCR
 Rat GDNFR α QSCSTKYRTLRLQCVAGKETNFSITSGLEAKDECRSAMEALKQKSLYNCR
 Human GRR2 SNCSSRYRTLRLQCLAGRDRN.....TMTLANKECQAALEVLQESPLYDCRC
 Rat GRR2 SNCSSRYRTLRLQCLAGRDRN.....TMTLANKECQAALEVLQESPLYDCRC

Human GDNFR α KRGMKKEKNCLRIYWSMYQSL.QGNDLLLEDSPYEPVNSRLSDIFRVVPFI
 Rat GDNFR α KRGMKKEKNCLRIYWSMYQSL.QGNDLLLEDSPYEPVNSRLSDIFRVVPFI
 Human GRR2 KRGMKKEQLCLQIYWSIHLGLTEGEFFYFASPYEPVTSRLSDIFRLASIF
 Rat GRR2 KRGMKKEQLCLQIYWSIHLGLTEGEFFYFASPYEPVTSRLSDIFRLASIF

1 2 5 / 1 3 5

FIG. 20B

Human GDNFR α
 Rat GDNFR α
 Human GRR2
 Rat GRR2

SDVFQQVEHI PKGNCLDAAKACNLDDI CKKYRSAYI TPCTTSVS .NDVC
 SDVFQQVEHISKGNCLDAAKACNLDDI CKKYRSAYI TPCTTSMS .NEVC
 SGTGADPVS AKSNHCLDAAKACNLNDN CKKLRSYISICNREISPTERC
 SGTGTDPAVSTKSNHCLDAAKACNLNDN CKKLRSYISICNREISPTERC

Human GDNFR α
 Rat GDNFR α
 Human GRR2
 Rat GRR2

NRRKCHKALRQFFDKVP AKHSYGM LFCSCRDIACTERRRQTI VPCSYEE
 NRRKCHKALRQFFDKVP AKHSYGM LFCSCRDIACTERRRQTI VPCSYEE
 NRRKCHKALRQFFDRVPSEYTYRM LFCSCQDQACAEERRRQTI LPSCSYED
 NRRKCHKALRQFFDRVPSEYTYRM LFCSCQDQACAEERRRQTI LPSCSYED

Human GDNFR α
 Rat GDNFR α
 Human GRR2
 Rat GRR2

REKPNCLNLQDSCKTNYICRSRLADFFTNCPESRSVSSCLKENYADCLL
 RERPNCLSLQDSCKTNYICRSRLADFFTNCPESRSVSNCLKENYADCLL
 KEKPNCLDLRGVCRTHL CRSRLADFFHANCRA SYQTIVISCPADNYQACILG
 KEKPNCLDLRSLCRTHL CRSRLADFFHANCRA SYRITISCPADNYQACILG

Human GDNFR α
 Rat GDNFR α
 Human GRR2
 Rat GRR2

AYSGLI GTVMTPNYIDSS . . SLSVAPWCD CSNBSGNDL EEC LKFLNFFKDN
 AYSGLI GTVMTPNYVDSS . . SLSVAPWCD CSNBSGNDL EDC LKFLNFFKDN
 SYAGMI GFDMTPNYVDSSPTGIVMSPWC SCRGSGNMEEECEKFLRDFTEN
 SYAGMI GFDMTPNYVDSSNPTGIVMSPWCNCRGSGNMEEECEKFLRDFTEN

FIG. 20C

Human GDNFR α
 Rat GDNFR α
 Human GRR2
 Rat GRR2

T	C	L	K	N	A	I	Q	A	F	G	N	G	S	D	V	I	V	W	Q	P	A	F	P	V	Q	T	I	A	T	T	T	A	L	R	V	K	N	K	P	I	G	P	A	G	S	E	N		
T	C	L	K	N	A	I	Q	A	F	G	N	G	S	D	V	I	V	W	Q	P	A	F	P	V	Q	T	I	A	T	T	T	A	L	R	V	K	N	K	P	I	G	P	A	G	S	E	N		
P	C	L	R	N	A	I	Q	A	F	G	N	G	I	N	V	N	V	S	P	K	G	P	S	F	Q	A	T	C	A	P	R	V	E	K	T	P	S	L	P	D	D	L	S	D	S	T	S	.	.
P	C	L	R	N	A	I	Q	A	F	G	N	G	I	N	V	N	V	S	P	K	G	P	S	L	P	A	T	C	A	P	R	V	E	K	T	P	S	L	P	D	D	L	S	D	S	T	S	.	.

Human GDNFR α
 Rat GDNFR α
 Human GRR2
 Rat GRR2

E	I	P	T	H	V	L	P	P	C	A	N	I	Q	A	Q	K	L	K	S	N	V	S	G	N	T	H	L	C	I	S	N	G	N	V	E	K	E	G	L	.	G	A	S	S	H	I	T	T	K	
E	I	P	T	H	V	L	P	P	C	A	N	I	Q	A	Q	K	L	K	S	N	V	S	G	S	T	H	L	C	I	S	D	S	D	F	G	K	D	C	I	A	G	A	S	S	H	I	T	T	K	
.	L	G	T	S	M	I	T	T	C	T	S	V	Q	E	Q	G	L	K	A	N	N	S	K	E	L	S	M	C	F	T	E	L	T	T	N	I	I	P	G	S	N	K	V	I	K	E	N	S	G	
.	L	G	T	S	M	I	T	T	C	T	S	I	Q	E	Q	G	L	K	A	N	N	S	K	E	L	S	M	C	F	T	E	L	T	T	N	I	I	S	P	G	S	K	K	V	I	K	E	N	S	G

Human GDNFR α
 Rat GDNFR α
 Human GRR2
 Rat GRR2

S	M	A	A	P	P	S	C	G	L	S	P	L	L	V	L	V	V	T	.	A	L	S	T	L	I	.	.	S	L	I	E	T	S
S	M	A	A	P	P	S	C	S	L	S	S	L	P	V	L	M	I	T	.	A	L	A	A	L	I	S	V	S	L	A	E	T	S
P	S	R	A	R	P	S	A	A	L	T	V	L	S	V	L	M	I	K	I	A	L												
S	S	R	A	R	P	S	A	A	L	T	A	L	P	L	L	M	I	T	A	L													

1 2 7 / 1 3 5

FIG. 21B

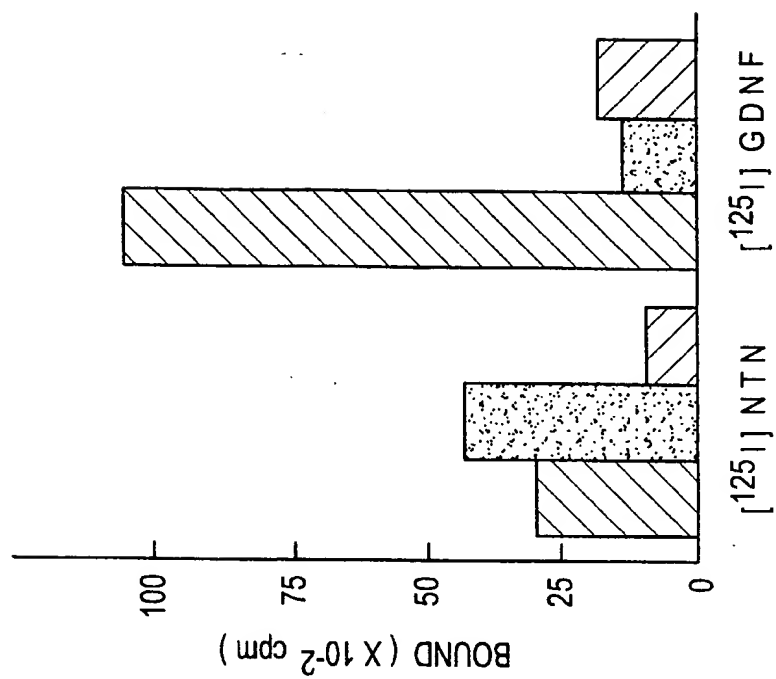
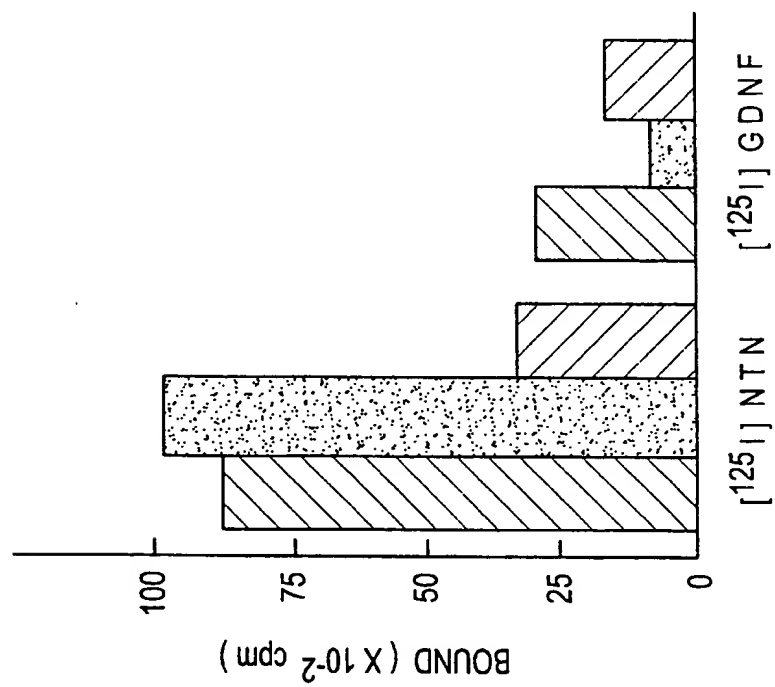
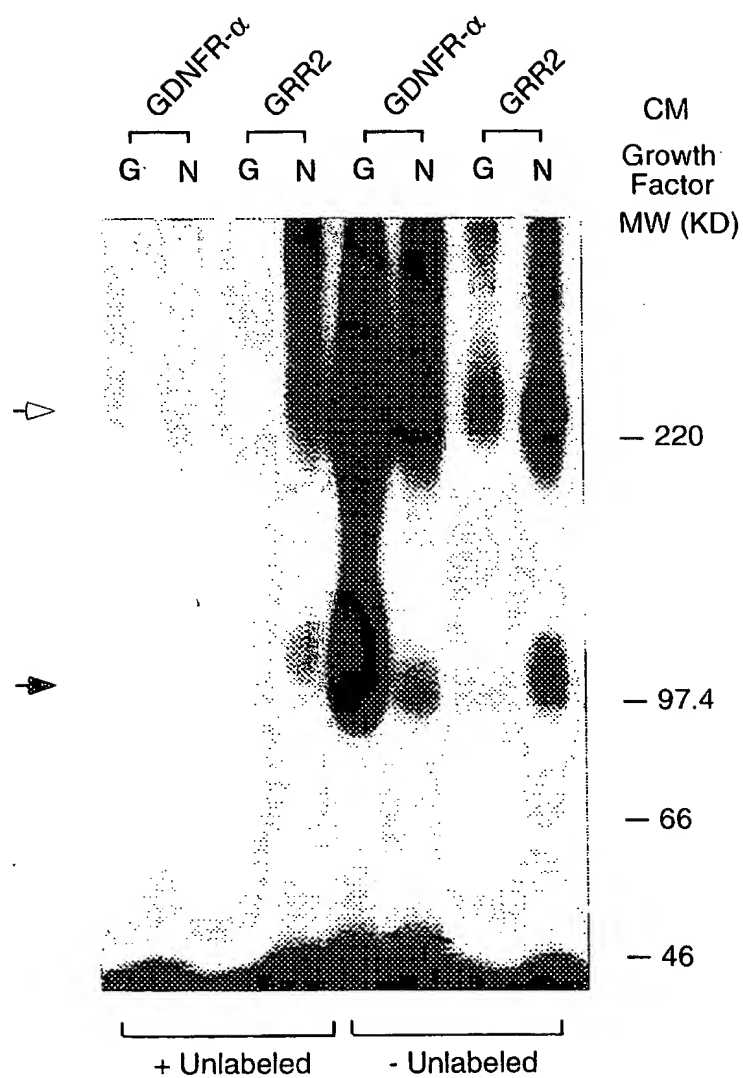


FIG. 21A



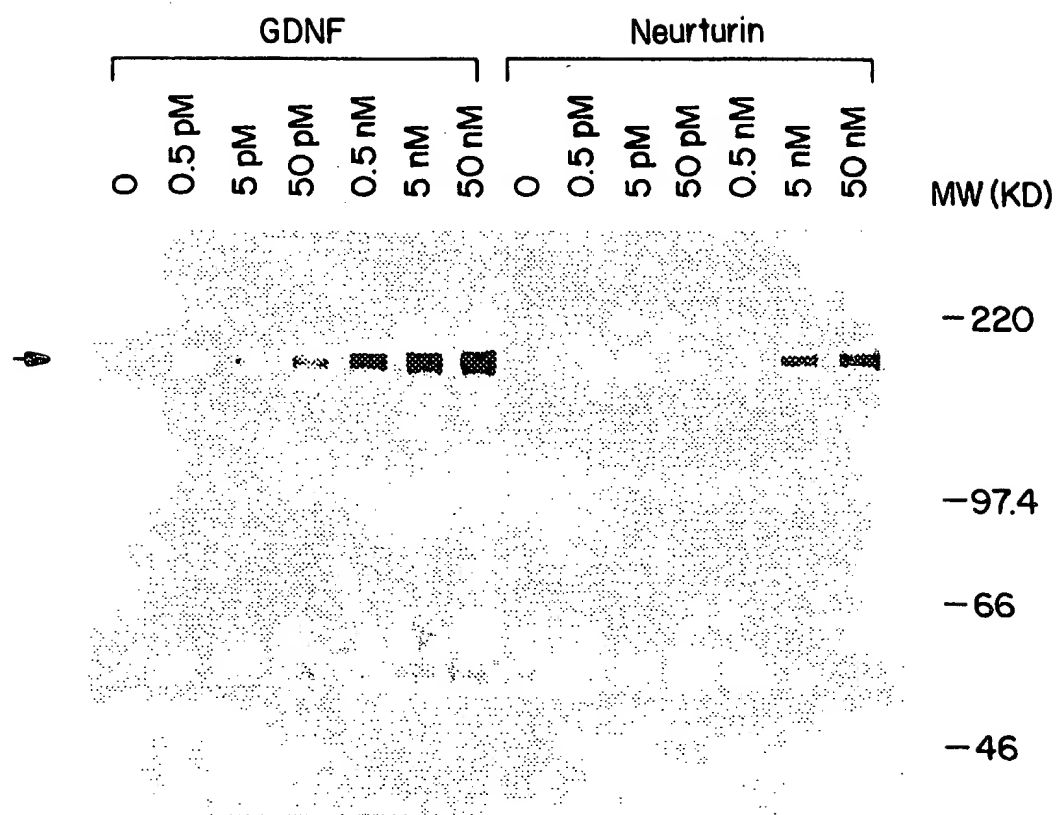
1 2 9 / 1 3 5

FIG.22



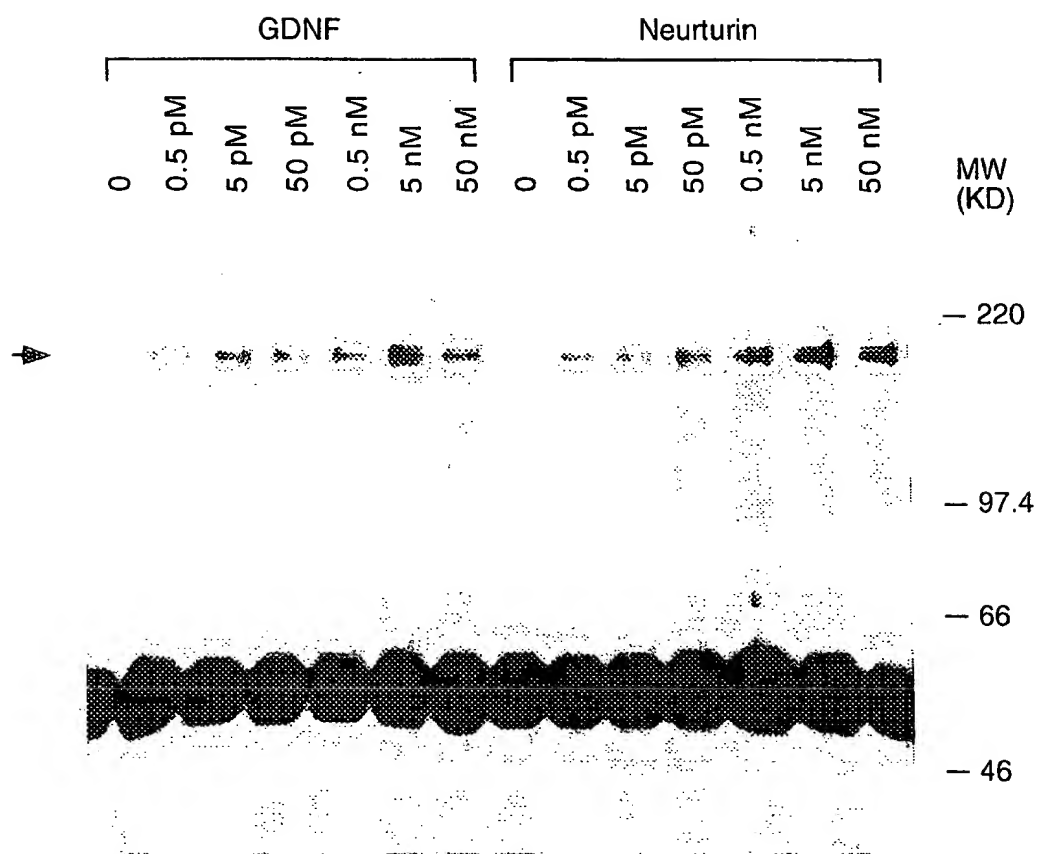
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FIG.23



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FIG.24



1 3 2 / 1 3 5

FIG.25

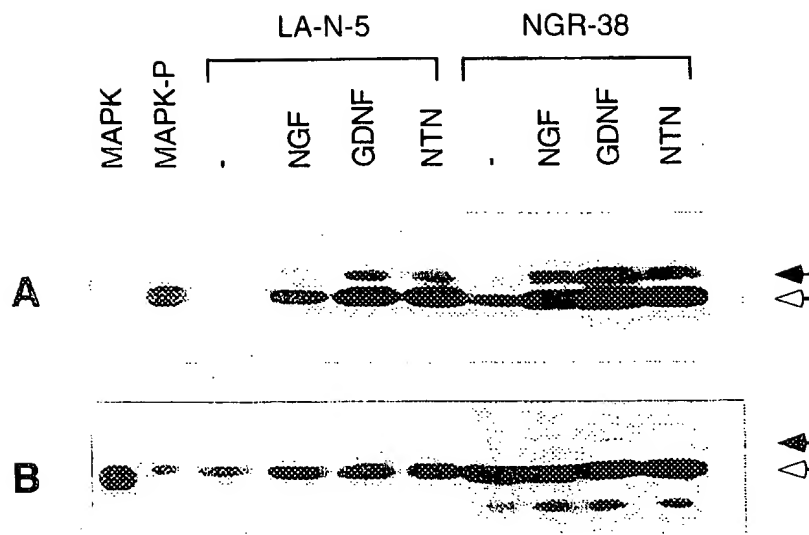


FIG. 26.A

1Pl.tl.s	1..pl.l..sr....d	50
CONSENSUS		..MFLATLYF	ALPLLDLLMS	AEVSGGDRLD	Cv.A....C.a
GDNFRMLVFP	SHYPDETLRS	LASPSSLQGS	ELHGWRPQVD	CVKASDQCLK
GRR2	MGLSRSPRPP	PLVILLLVLS	LWLPLGTGNS	LPTENRLVNS	CVRANELCAA
GRR3					CTQARKKCEA
51	e..Cs..Yrt	LrqC.ag...	n.....a	..eC..A.e.	100
CONSENSUS	EQSCSTKYRT	LRQCVAGKET	NFSLTSGLEA	KDECRSAMEA	L..sslydCR
GDNFR	ESNCSSRYRT	LRQCLAGRDR	N....TMLA	NKECQAALEV	LKQKSLYNCR
GRR2	NPACKAAYQH	LDSCTPSLSS	PLPSGES.AT	SAACLEAAQQ	LQESPLYDCR
GRR3					LRNSSLIDCR
101	CkRgMKke..	CL.IYws.h.	.l..G....le	.SPYE.pvts	150
CONSENSUS	CKRGMKKEKN	CLRIYWSMYQ	SL.QGNDLLE	DSPYE.PVNS	rlsdiFr...s
GDNFR	CKRGMKKELQ	CLQIYWSIHL	GLTEGEEFYE	ASPYE.PVTS	RLSDIFRAVP
GRR2	CHRRMKHQAT	CLDIYWTVHP	VRSLGDYELD	VSPYEDTVTS	RLSDIFRLAS
GRR3					..KPKWMNLS

FIG. 26.B

151	..S....d... FISDVFFQVE IFSGTGTDP KLSMLKPD..	...ksn.CLD HISKGNCLD VSTKSNHCLDSDLCLK	aAkaCnLnD. AAKACNLDDT AAKACNLNDN FAMLCNLNDK	CkklRsaYi. CKKYRSAYIT CKKLRSSYIS CDRLRKAYGE	.C....S...e PCTTSM.S.NE ICNREISPTE AC....SG.I	200
201	rCnRrkChka VCNRRKCHKA RCNRRKCHKA RCQRHLCLAQ	LRqFFdkvp. LRQFFDKVPA LRQFFDRVPS LRSFFEKAAE	.h.ygmLfCs KHSYGMLFCS EYTYRMLFCS SHAQGLLLCP	C...D.aC.E C...RDIACTE C...QDQACAE CAPEDAGCGE	RRRqTI.PsC RRRQTIVPVC RRRQTILPSC RRRNTIAPSC	250
251	syE...e.PNC SYEERERPNC SYEDKEKPNC ALPSVA.PNC	LdLrs.CrtD LSLQDSCKTN LDLRSLCRTD LDLRSFCRAD	.lCRSRLaDF YICRSRLADF HLCRSRLADF PLCRSRLMDF	.tnC.p...r. FTNCQPEsRS HANCRASTRT QTHCHPMDIL	.t.C.a.ny. VSNCLKENYA ITSCPADNYQ GT.C.ATEQS	300
301	.CL.aY.GLI DCLLAYSGLI ACLGSYAGMI RCLRAYLGLI	Gt.MTPNyvd GTVMTPNYVD GFDMPNYVD GTAMTPNFIS	s...t....Vap SSSL...SVAP SNPTGIVVSP KVNTT...VAL	wC.CrgSGN. WCDCSNSGND WCNCRGSGNM GCTCRGSGNL	.eeCekf1.. LEDCLKFLNF EECEKFLRD QDECEQLEKS	350

CONSENSUS
GDNFR
GRR2
GRR3

CONSENSUS
GDNFR
GRR2
GRR3

CONSENSUS
GDNFR
GRR2
GRR3

CONSENSUS
GDNFR
GRR2
GRR3

FIG. 26.C

351	CONSENSUS	F..NpCL.nA	IqAfgng.dv	.msq..p...	.t.a.....	400
	GDNFR	FKDNTCLKNA	IQAFNGSDV	TMWQPAPPVQ	TTTATTTTAF	RVKNKP.LGP
	GRR2	FTENPCLRNA	IQAFNGTDDV	NMSPKGPSLP	ATQAP.....	RVEKTPSLPD
	GRR3	FSQNPCLMEA	IAAKMRFHRQ	LFSQDWADST	FSVMQQQNSS	PALRPQ.....
401	CONSENSUS	..S.....t	.v...c...q	.q.lk.n.s.C.....	450
	GDNFR	AGS.ENEIPT	HVLPPCANLQ	AQKLKSNVSG	STHLCLSDSD	FGKDGLAGAS
	GRR2	DLSDSTSLGT	SVITTCSTIQ	EQGLKANNSK	ELSMCFTELT	TNISPGSKKV
	GRR3
451	CONSENSUSs...a	..s...l...LP	vLmlt.1....	1....1.ets	489
	GDNFR	SHITTKSMAA	PPCSLSSLP	VLMLTALAAL	LSVSLAETS	
	GRR2	IKLNSGSSRA	RLSAALTALP	LLMLTLAL	LLQTLW	
	GRR3LRLP	VLSFFILTLL		

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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C12N 15/12, C07K 14/71, A61K 38/17, C07K 16/28	A3	(11) International Publication Number: WO 98/54213 (43) International Publication Date: 3 December 1998 (03.12.98)
(21) International Application Number: PCT/US98/08486 (22) International Filing Date: 27 April 1998 (27.04.98) (30) Priority Data: 08/866,354 30 May 1997 (30.05.97) US (71) Applicant: AMGEN INC. [US/US]; Amgen Center, One Amgen Center Drive, Thousand Oaks, CA 91320-1789 (US). (72) Inventors: FOX, Gary, M.; 35 West Kelly Road, Newbury Park, CA 91320 (US). JING, Shuqian; 3254 Bordero Lane, Thousand Oaks, CA 91362 (US). WEN, Duanzhi; 517 Raindance Street, Thousand Oaks, CA 91360 (US). (74) Agents: ODRE, Steven, M. et al.; Amgen Inc., Amgen Center, One Amgen Center Drive, Thousand Oaks, CA 91320-1789 (US).		(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i> (88) Date of publication of the international search report: 7 January 1999 (07.01.99)
(54) Title: NEUROTROPHIC FACTOR RECEPTORS		
(57) Abstract <p>The present invention relates to glial cell line-derived neurotrophic factor (GDNF), a potent neurotrophin that exhibits a broad spectrum of biological activities on a variety of cell types from both the central and peripheral nervous systems. The present invention involves the cloning and characterization of receptors for GDNF. Nucleic acid and amino acid sequences are described for GDNFR protein products. A hydrophobic domain with the features of a signal peptide is found at the amino terminus, while a second hydrophobic domain at the carboxy terminus is involved in the linkage of the receptor to the cell membrane. The lack of a transmembrane domain and cytoplasmic region indicates that GDNFR requires one or more accessory molecules in order to mediate transmembrane signaling. GDNFR mRNA is widely distributed in both nervous system and non-neural tissues, consistent with the similar distribution found for GDNF.</p>		

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INTERNATIONAL SEARCH REPORT

International Search No.
PCT/US 98/08486

A. CLASSIFICATION OF SUBJECT MATTER
IPC 6 C12N15/12 C07K14/71 A61K38/17 C07K16/28

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 6 C12N C07K A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	JING S ET AL: "GDNF-INDUCED ACTIVATION OF THE RET PROTEIN TYROSINE KINASE IS MEDIATED BY GDNFR-ALPHA, A NOVEL RECEPTOR FOR GDNF" CELL, vol. 85, 28 June 1996, pages 1113-1124, XP002036435	1,2,4-6, 9-11, 13-15, 17-29, 31-35, 51,53-60
Y	see the whole document	41-44, 46-50, 62-66
	--- -/--	

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

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Date of the actual completion of the international search

4 November 1998

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INTERNATIONAL SEARCH REPORT

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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No. *
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INTERNATIONAL SEARCH REPORT

International Application No.
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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No. .
P,X	WO 97 40152 A (AMGEN INC) 30 October 1997 see the whole document ---	1,2,4-6, 9-15, 17-29, 31-48, 51-64
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INTERNATIONAL SEARCH REPORT

International Application No.
PCT/US 98/08486

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

Although claims 37-40 and 61 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☒ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☒ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 2-8,15,16,29,30, and 1,9-14,17-28,31-48, 51-64 partially.

Human, rat and murine GDNFR-alpha, or a protein comprising a significant portion thereof, nucleic acids encoding them and (expression) vectors containing one of the nucleic acids, pharmaceutical compositions containing one of the proteins, host cells transformed with these vectors, method for producing the proteins using the host cells, device for treating nerve damage comprising recombinant cells expressing one of the proteins, surrounded by a semipermeable membrane, use of a pharmaceutical composition comprising one of the proteins for the treatment of improperly functioning dopaminergic nerve cells, Parkinson's disease, Alzheimer's disease, and amyotrophic lateral sclerosis, antibodies against the proteins and hybridoma cells producing them.

2. Claims: 1,9-14,17-28,31-48,51-64 partially.

A protein comprising seq. 36 (human GRR2) or seq. 40 (rat GGR2), nucleic acids encoding these proteins and (expression) vectors containing the nucleic acids, pharmaceutical composition containing one of the proteins, host cell transformed with one of the vectors, method for producing one of the proteins using the host cell, device for treating nerve damage comprising recombinant cells expressing one of the proteins, surrounded by a semipermeable membrane, use of a pharmaceutical composition comprising one of the proteins for the treatment of improperly functioning dopaminergic nerve cells, antibodies against the proteins and hybridoma cells producing them, device for treating nerve damage comprising an implantable semipermeable capsule containing the host cells expressing one of the proteins.

3. Claims: 1,9-14,17-28,31-48,51-64 partially.

A protein comprising seq. 38 (human GRR3) or seq. 42 (rat GGR3), nucleic acids encoding these proteins and (expression) vectors containing the nucleic acids, pharmaceutical composition containing one of the proteins, host cell transformed with one of the vectors, method for producing one of the proteins using the host cell, device for treating nerve damage comprising recombinant cells expressing one of the proteins, surrounded by a semipermeable membrane, use of a pharmaceutical composition comprising one of the proteins for the treatment of improperly functioning dopaminergic nerve cells, antibodies

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

against the proteins and hybridoma cells producing them, device for treating nerve damage comprising an implantable semipermeable capsule containing the host cells expressing one of the proteins.

4. Claims: 49,50,65,66

Device for analysing the presence of a neurotrophic factor in a sample comprising a solid phase coated with a GDNFR protein which reacts with said neurotrophic factor, and a method of analysis using said device.

5. Claims: 67-69

Method for determining whether a ligand activates a receptor tyrosine kinase, whereby said ligand and receptor tyrosine kinase and a GDNFR are contacted, and activation is monitored.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 98/08486

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